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 WISE (TM)  
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Run on: Wed Aug 16 09:32:39 2000; MasPar time 20.12 Seconds  
 768.349 Million cell updates/sec

Tabular output not generated.

Title: >US-09-416-267-2  
 Description: (1-223) from US09416267.pep  
 Perfect Score: 1738  
 Sequence: 1 MKLHVAVLTALILMFLTWL.....IGPECIDYSGKTVKCMCMF 223

Scoring table: PAM 150  
 Gap 11

Searched: 225878 segs, 69334122 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database:

sptrembl12  
 1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human  
 5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle  
 9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified  
 13:sp-vertebrate 14:sp-virus

Statistics: Mean 43.035; Variance 77.012; scale 0.555

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	102	5.9	417	10	664618	6.42e+02
2	103	5.9	434	11	089030	4.57e+02
3	102	5.9	640	11	009182	6.42e+02
4	100	5.8	417	4	09Y409	1.26e+01
5	100	5.8	633	5	022468	1.26e+01
6	98	5.6	1360	10	092VU3	2.45e+01
7	95	5.5	439	4	016042	6.54e+01
8	95	5.5	596	4	095612	6.54e+01
9	94	5.4	246	4	099750	9.02e+01
10	93	5.4	756	5	044417	1.24e+00
11	93	5.4	1454	14	066928	1.24e+00
12	94	5.4	2100	5	021281	9.02e+01
13	92	5.3	1096	3	014022	1.71e+00
14	90	5.2	40	14	057150	3.19e+00
15	90	5.2	116	2	09X2C3	3.19e+00
16	90	5.2	157	11	062331	3.19e+00
17	90	5.2	241	5	022205	3.19e+00
18	90	5.2	343	13	042607	3.19e+00
19	91	5.2	618	3	006817	2.34e+00
20	91	5.2	690	3	006993	2.34e+00

## ALIGNMENTS

RESULT ID	1	PRELIMINARY:	PRT:	417 AA.	SPECIAL LOBE-SPECIFIC PUTATIVE MEMBRANE-ASSO	2.34e+00
AC 064618	01-AUG-1998 (TREMBLrel. 07, Created)				3.19e+00	
DR 01-NOV-1998 (TREMBLrel. 07, Last sequence update)					3.19e+00	
DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)					3.19e+00	
DE F19P24.8 PROTEIN.					3.19e+00	
OS Arabidopsis thaliana (Mouse-ear cross).					3.19e+00	
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					3.19e+00	
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;					3.19e+00	
OC core eudicots; Rosidae; eustosids II; Brassicales; Brassicaceae;					3.19e+00	
OC Arabidopsis.					3.19e+00	
RN [1]					3.19e+00	
RP SEQUENCE FROM N.A.					3.19e+00	
RC STRAIN-CV. COLUMBIA;					3.19e+00	
RA ROUSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,					3.19e+00	
RA SYKES S.M., KAUL S., MASON T.M., KERLAJAGE A.R., ADAMS M.D.,					3.19e+00	
RA SOMERVILLE C.R., VENTER J.C.,					3.19e+00	
RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.					3.19e+00	
DR EMBL: AC003673; AAC09024.1;					3.19e+00	
DR MENDEL; 28581; Arabid;3412;28581.					3.19e+00	
DR PFAM: PF00041; fn3; 1.					3.19e+00	
SO SEQUENCE 417 AA; 47607 MW; 6A31B808 CRC32;					3.19e+00	
Query Match	5.9%	Score 102;	DB 10;	Length 417;		
Best Local Similarity	27.5%	Pred. No. 6.42e+02;				
Matches	22;	Conservative	20;	Mismatches	34;	Indels
					4;	Gaps
					4;	
DB 273 WFKVFSGEVSELSDEFVS-TKTLDEEVAVALNNSNCNANKMKSGSCSPG-FEE 330						
QY 116 W-NIVSFPAEELSHENLVSLFETVNPQPHONVSPVSNNAHAPRSSDKEMHCIVYVYDD 174						
DB 331 CYNLIR-QLECSGQVKSDFR 349						
QY 175 CMSIHCKISCESMGASKYR 194						
RESULT 2						
ID 089030	PRELIMINARY:	PRT:	434 AA.			
AC 089030;						
DT 01-NOV-1998 (TREMBLrel. 08, Created)						
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)						
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)						

DE MATRILIN-4 PRECURSOR, ALTERNATE SPLICE PRODUCT.  
 GN MAT-4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN-C57BL/6J; TISSUE-TOTAL FOETUS;  
 RX MEDLINE: 98442849.  
 RA WAGNER R., KOBBE B., PAULSON M.;  
 RT Matrilin-4, a new member of the matrilin family of extracellular  
 RT matrix proteins.  
 RL FEBS Lett. 436:123-127(1998).  
 DR EMBL: AJ006140; CAA06890.1; .  
 DR HSSP: P00736; IAP0.  
 DR PROSITE: PS00010; ASX\_HYDROXYL. 2.  
 DR PFAM: PF00008; EGF. 4.  
 DR PFAM: PF00092; vwa; 1.  
 DR PRINTS: PR00453; VMPADOMAIN.  
 KW Signal; Glycoprotein; EGF-like domain.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 434 MATRILIN-4 PRECURSOR.  
 FT CHAIN 22 434 MATRILIN-4 PRECURSOR, ALTERNATE SPLICE  
 FT VARIANT 129 129 PRODUCT.  
 FT VARIANT 156 156 A -> E.  
 FT VARIANT 156 156 G -> D.  
 SQ SEQUENCE 434 AA; 47944 MW; B29D559A CRC32;  
 Query Match 5.9%; Score 103; DB 11; Length 434;  
 Best Local Similarity 41.7%; Pred. No. 4,576-02;  
 Matches 20; Conservative 6; Mismatches 18; Indels 4; Gaps 3;  
 Db 9 LSL-LTFLFOSWETOLOSAGKDLCAELVHG--OHLGNMAGTFYAC 53  
 QY 9 LTLALIMFL-TWLPESLSCNKLACSDVSKLIQELCCRPBGNCSC 55  
 RESULT 3  
 ID 009182; PRELIMINARY; PRT; 640 AA.  
 AC 009182;  
 DT 01-JUL-1997 (TREMblrel. 04, Created)  
 DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)  
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)  
 DE INTEGRIN BETA-7 SUBUNIT (FRAGMENT).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-SPRAGUE-DAWLEY; TISSUE-SPLEEN;  
 RT TIDSWELL M., PACHYNSKI R., WU S.W., QIU S.O., DUNHAM E., COCHRAN N.,  
 RT BRISKIN M.J., KILSHAW P.J., LAZAROVITS A.I., ANDREW D.P.,  
 RA BUTCHER E.C., YEDNOCK T.A., ERLE D.J.;  
 RL J. Immunol. 0:0-0(0).  
 CC -1- FUNCTION: INTEGRINS ARE A LARGE FAMILY OF CELL SURFACE  
 CC GLYCOPROTEINS THAT MEDIATE CELL TO CELL & CELL TO MATRIX ADHESION.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: WITH OTHER BETA CHAINS FROM THE INTEGRIN FAMILY OF  
 CC CELL-SURFACE RECEPTOR.  
 DR EMBL: AF003598; AAB61241.1; .  
 DR PROSITE: PS00243; INTEGRIN\_BETA. 3.  
 DR PFAM: PF00362; Integrin\_B. 1.  
 DR Integrin; Cell adhesion; Transmembrane; Glycoprotein; Repeat.  
 FT NON\_TER 1  
 SQ SEQUENCE 640 AA; 69015 MW; 313C3A97 CRC32;  
 Query Match 5.9%; Score 102; DB 11; Length 640;  
 Best Local Similarity 31.6%; Pred. No. 6,426-02;  
 Matches 18; Conservative 13; Mismatches 22; Indels 4; Gaps 4;  
 Db 432 CSEVSDVSCVSEGGIC-GSGHGDCKNRCQCLDGYGALCDCLCKSPCEYRDCAE 487  
 QY 31 CASDVSKLIQELCCRPBGNCSCCK-ECN-LCLGALIMPECCVCVGMCP-RKYS D 84

DE MATRILIN-4 PRECURSOR, ALTERNATE SPLICE PRODUCT.  
 GN MAT-4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN-C57BL/6J; TISSUE-TOTAL FOETUS;  
 RX MEDLINE: 98442849.  
 RA WAGNER R., KOBBE B., PAULSON M.;  
 RT Matrilin-4, a new member of the matrilin family of extracellular  
 RT matrix proteins.  
 RL FEBS Lett. 436:123-127(1998).  
 DR EMBL: AJ006140; CAA06890.1; .  
 DR HSSP: P00736; IAP0.  
 DR PROSITE: PS00010; ASX\_HYDROXYL. 2.  
 DR PFAM: PF00008; EGF. 4.  
 DR PFAM: PF00092; vwa; 1.  
 DR PRINTS: PR00453; VMPADOMAIN.  
 KW Signal; Glycoprotein; EGF-like domain.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 434 MATRILIN-4 PRECURSOR.  
 FT CHAIN 22 434 MATRILIN-4 PRECURSOR, ALTERNATE SPLICE  
 FT VARIANT 129 129 PRODUCT.  
 FT VARIANT 156 156 A -> E.  
 FT VARIANT 156 156 G -> D.  
 SQ SEQUENCE 434 AA; 47944 MW; B29D559A CRC32;  
 Query Match 5.9%; Score 103; DB 11; Length 434;  
 Best Local Similarity 41.7%; Pred. No. 4,576-02;  
 Matches 20; Conservative 6; Mismatches 18; Indels 4; Gaps 3;  
 Db 9 LSL-LTFLFOSWETOLOSAGKDLCAELVHG--OHLGNMAGTFYAC 53  
 QY 9 LTLALIMFL-TWLPESLSCNKLACSDVSKLIQELCCRPBGNCSC 55  
 RESULT 3  
 ID 009182; PRELIMINARY; PRT; 640 AA.  
 AC 009182;  
 DT 01-JUL-1997 (TREMblrel. 04, Created)  
 DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)  
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)  
 DE INTEGRIN BETA-7 SUBUNIT (FRAGMENT).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-SPRAGUE-DAWLEY; TISSUE-SPLEEN;  
 RT TIDSWELL M., PACHYNSKI R., WU S.W., QIU S.O., DUNHAM E., COCHRAN N.,  
 RT BRISKIN M.J., KILSHAW P.J., LAZAROVITS A.I., ANDREW D.P.,  
 RA BUTCHER E.C., YEDNOCK T.A., ERLE D.J.;  
 RL J. Immunol. 0:0-0(0).  
 CC -1- FUNCTION: INTEGRINS ARE A LARGE FAMILY OF CELL SURFACE  
 CC GLYCOPROTEINS THAT MEDIATE CELL TO CELL & CELL TO MATRIX ADHESION.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: WITH OTHER BETA CHAINS FROM THE INTEGRIN FAMILY OF  
 CC CELL-SURFACE RECEPTOR.  
 DR EMBL: AF003598; AAB61241.1; .  
 DR PROSITE: PS00243; INTEGRIN\_BETA. 3.  
 DR PFAM: PF00362; Integrin\_B. 1.  
 DR Integrin; Cell adhesion; Transmembrane; Glycoprotein; Repeat.  
 FT NON\_TER 1  
 SQ SEQUENCE 640 AA; 69015 MW; 313C3A97 CRC32;  
 Query Match 5.9%; Score 102; DB 11; Length 640;  
 Best Local Similarity 31.6%; Pred. No. 6,426-02;  
 Matches 18; Conservative 13; Mismatches 22; Indels 4; Gaps 4;  
 Db 432 CSEVSDVSCVSEGGIC-GSGHGDCKNRCQCLDGYGALCDCLCKSPCEYRDCAE 487  
 QY 31 CASDVSKLIQELCCRPBGNCSCCK-ECN-LCLGALIMPECCVCVGMCP-RKYS D 84

Db 494 ITWYSDAGEKRCGRDVP-LEGEAPTCNPDANAHCCSGCYC-GNSKEHCECNGC 551  
 17 LTMV-PELSCNKAICADVSKLIDELCCRCRPGECNCSCKECLGALMBEC-CD-C 73  
 QY 552 IDFAKORDFKYK 564

QY 74 VGMCPNRYSDPT 86

RESULT 6 PRELIMINARY: PRT: 1360 AA.

AC 092V03;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)  
 DE T5A14.15 PROTEIN.

Arabidopsis thaliana (Mouse-ear cress).  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 euophyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;  
 core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;  
 Arabidopsis.

[1]  
 SEQUENCE FROM N.A.  
 RA FEDERSPIEL N.A., PALM C.J., CONWAY A.B., CONN L., HANSEN N.F.,  
 RA ALTAFFI H., ARAUJO R., HUIZAR L., ROWLEY D., BUEHLER E., DUNN P.,  
 RA GONZALEZ A., KREMETSCHKA I., KIM C., LENZ C., LI J., LIU S.,  
 RA LUKERS S., SCHWARTZ J., SHINN P., TORIUMI M., VYSOTSKAIA V.S.,  
 RA WALKER M., XU G., ECKER J., THEOLOGIS A., DAVIS R.W.,  
 RA Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: AC005223; AADI0650.1;  
 DR EMBL: AC005223; AADI0650.1;  
 SQ SEQUENCE 1360 AA; 154661 MW; A7040DF1 CRC32;

Query Match 5.6%; Score 98; DB 10; Length 1360;  
 Best Local Similarity 31.9%; Pred. No. 2.45e-01;  
 Matches 22; Conservative 12; Mismatches 29; Indels 6; Gaps 6;

Db 1218 FLECIKCKSFGLKATLPSEAHYRHRRL-TLCY-RDYMTSHHMCET-CESK-LSITY 1273  
 QY 136 FLEIYNQHNQNVSPSNVNAIPSSDKENHCTVYFPDCKSHQ-CIKSESGAKSKYR 194

Db 1274 WFT-TCDSK 1281  
 QY 195 WFNACCEC 203

RESULT 7 PRELIMINARY: PRT: 439 AA.

AC 016042;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR.

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

[1]  
 SEQUENCE FROM N.A.  
 RA MEDLINE: 91370690.  
 RA DEMBIC Z., LOETSCHER H., GUBLER U., PAN Y.C., LAHM H.W., GENTZ R.,  
 RA BROCKHAUS M., LESSLAUER W.;  
 RT "Two human TNF receptors have similar extracellular, but distinct  
 RT intracellular, domain sequences."  
 RT Cytokine 2:231-237(1990).

DR EMBL: S63368; AAB19824.1;  
 DR HSBP: P25942; ICDP.  
 DR PROSITE: PS00652; TNFR\_NGFR.1; 2.  
 DR PFM: PF00020; TNFR\_C6; 4.  
 SQ SEQUENCE 439 AA; 46090 MW; 1CE766FB CRC32;

Query Match 5.5%; Score 95; DB 4; Length 439;  
 Best Local Similarity 42.4%; Pred. No. 6.54e-01;

Matches 25; Conservative 10; Mismatches 13; Indels 11; Gaps 11;  
 Db 67 WPEELSCG-SRCSDDYETQACTREONRICTRPG-WYCALSKOEGCRLC-APLRK-C 121  
 QY 19 WPELSCNKAICADVSKLIDELCCRCRPGECNCSCKECLGALMBEC 70

RESULT 8 PRELIMINARY: PRT: 596 AA.

AC P95612;  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)  
 DE MODULATION PROTEIN.  
 GN NOLX.

OS Rhizobium fredii.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Sinorhizobium.

[1]  
 SEQUENCE FROM N.A.  
 RA STRAIN-USDAL91;  
 RA BELLATO C., KRISHNAN H.B., CUBO T., VERA F.T., PUEPPRE S.G.;  
 RL Microbiology 0:0-0(0).  
 DR EMBL: U77701; AAB19229.1;  
 SQ SEQUENCE 596 AA; 64012 MW; CF154622 CRC32;

Query Match 5.5%; Score 95; DB 2; Length 596;  
 Best Local Similarity 29.9%; Pred. No. 6.54e-01;  
 Matches 23; Conservative 21; Mismatches 30; Indels 3; Gaps 3;

Db 156 PSTPPLKAIEFLD-PELFYAGSGDGRGGRKIRAKDSESKHHPOVAARQESA 214  
 QY 83 SDTPPTSKSTVELEIPSLFRAL-TEDGTQLMNNIVSFVAELSHENLVSLFTVN 141

Db 215 QSYAONY-IPSDSAENA 230  
 QY 142 QPHQNVSPSNVNAIP 158

RESULT 9 PRELIMINARY: PRT: 246 AA.

AC 099750;  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
 DE MYOGENIC REPRESSOR I-MF.

GN MDT.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

[1]  
 SEQUENCE FROM N.A.  
 RA TISSUE-BRAIN;  
 RX MEDLINE: 96390847.  
 RA CHEN C.M., KRAAT N., GROUNDINE M., WEINTRAUB H.;  
 RT "I-MF, a novel myogenic repressor, interacts with members of the MyoD  
 RT family."  
 RT Cell 86:731-741(1996).

DR EMBL: U78313; AAB39748.1;  
 DR EMBL: U78313; AAB39748.1;  
 SQ SEQUENCE 246 AA; 25029 MW; 0CD862A7 CRC32;

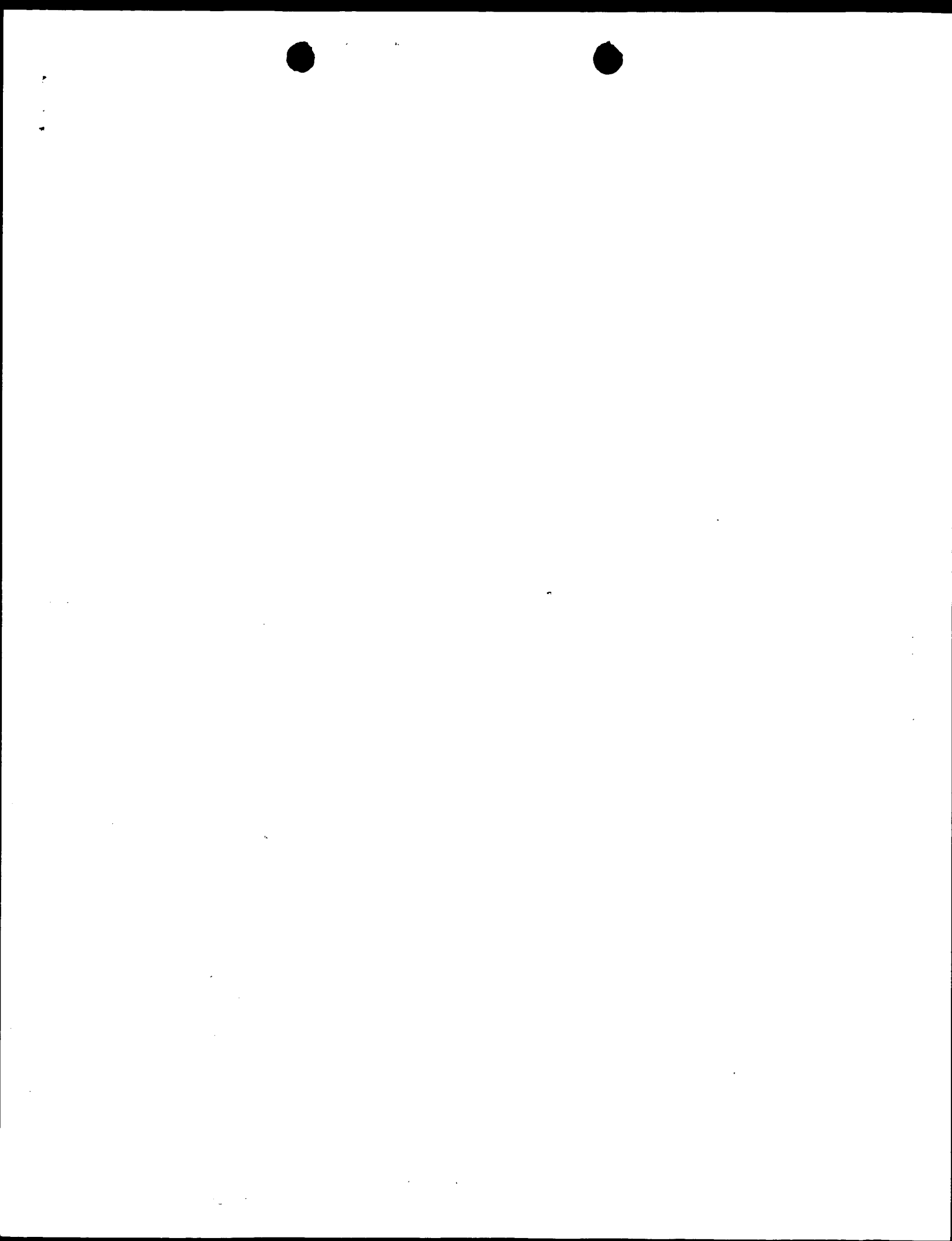
Query Match 5.4%; Score 94; DB 4; Length 246;  
 Best Local Similarity 38.7%; Pred. No. 9.02e-01;  
 Matches 24; Conservative 8; Mismatches 20; Indels 10; Gaps 9;

Db 175 EPLTICNIVIDCAT-GGSCSSESCICCCCGSGCAGADDDPCDDC-GIL-DACCESAD 231  
 QY 22 ESLS-CKAL-CASDVSKLIDELCCRCRPGECNCSCKECLGALMBECDCV 75

Db 232 -C 232  
 QY 76 MC 77







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 W P S E R F I  
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ch\_pp protein - protein database search, using Smith-Waterman algorithm  
 Run on: Wed Aug 16 09:31:40 2000; Maspar time 8.67 Seconds  
 796.748 Million cell updates/sec  
 Tabular output not generated.

Title: >US-09-416-267-2  
 Description: (1-223) from US09416267.pep  
 Perfect score: 1738  
 Sequence: 1 MKLHVAVLTALIMELTWL.....ISPECIDYGSKTVCNMCNF 223

Scoring table:  
 PAM 150  
 Gap 11

Searched: 85661 seqs, 30989116 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: swiss-prot38  
 1:swissprot

Statistics: Mean 44.527; Variance 72.235; scale 0.616

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	537	30.9	249	1	TSG_DROME TWISTED GASTRULATION P	4.07e-100
2	104	6.0	798	1	ITB7_HUMAN INTEGRIN BETA-7 PRECUR	7.22e-03
3	101	5.8	194	1	COX2_PARDE PROBABLE CYTOCHROME C	2.16e-02
4	97	5.6	243	1	GTI2_MOUSE GLUTATHIONE S-TRANSFER	8.98e-02
5	97	5.6	806	1	ITB7_MOUSE INTEGRIN BETA-7 PRECUR	8.98e-02
6	96	5.5	1799	1	LMB2_MOUSE LAMININ BETA-2 CHAIN P	1.27e-01
7	96	5.5	326	1	AAIR_BOVIN ADENOSINE A1 RECEPTOR	1.27e-01
8	96	5.5	461	1	CLUS_PIG CLUSTERIN PRECURSOR (C	1.27e-01
9	95	5.5	461	1	TNR2_HUMAN TUNOR NECROSIS FACTOR	1.80e-01
10	95	5.5	471	1	NOLX_RHIFR NODULATION PROTEIN NOL	1.80e-01
11	96	5.5	1801	1	LMB2_RAT LAMININ BETA-2 CHAIN P	1.27e-01
12	96	5.5	3084	1	LMB2_MOUSE LAMININ BETA-2 CHAIN P	1.27e-01
13	94	5.4	62	1	MT_XENLA METALLOTHIONEIN	2.54e-01
14	93	5.4	596	1	NOLX_RHISN NODULATION PROTEIN NOL	2.54e-01
15	94	5.4	3075	1	LMB1_HUMAN LAMININ ALPHA-1 CHAIN	2.54e-01
16	92	5.3	130	1	YK06_YEAST HYPOTHETICAL 14.9 KDA	5.02e-01
17	92	5.3	538	1	MEMBRANE TRANSPORTER D	5.02e-01
18	92	5.3	1096	1	ATCY_SCHPO PROBABLE CATION-TRANSP	5.02e-01
19	90	5.2	63	1	MTI_COLLI METALLOTHIONEIN-1 (MT-	9.81e-01
20	90	5.2	167	1	Y109_MYCG HYPOTHETICAL PROTEIN M	9.81e-01
21	90	5.2	324	1	AAIR_CHICK ADENOSINE A1 RECEPTOR	9.81e-01
22	91	5.2	445	1	CLUS_CANFA CLUSTERIN PRECURSOR (G	7.03e-01
23	90	5.2	690	1	AFI1_YEAST IRON-REGULATED TRANSCR	9.81e-01

RESULT ID	1	STANDARD	PRT	249 AA.	ALIGNMENTS
AC	PS4356:				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	01-NOV-1997 (Rel. 35, Last annotation update)				
DE	TWISTED GASTRULATION PROTEIN PRECURSOR				
GN	TSG.				
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OC	Ephydroidea; Drosophilidae; Drosophila.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-EMBRYO.				
RX	MEDLINE: 95047309.				
RA	Mason E.D., Konrad K.D., Webb C.D., Marsh J.L.;				
RT	"Dorsal midline fate in Drosophila embryos requires twisted				
RT	gastrulation, a gene encoding a secreted protein related to human				
RT	connective tissue growth factor.";				
RL	Genes Dev. 8:1489-1501(1994).				
CC	-1- FUNCTION: SPECIFY THE FATE OF DORSAL CELLS IN DROSOPHILA EMBRYOS.				
CC	MUTATIONS OF TSG ONLY AFFECT THE FATE OF A NARROW STRIP OF DORSAL				
CC	MIDLINE CELLS AND DO NOT AFFECT DORSAL ECTODERM CELLS.				
CC	-1- SIMILARITY: SOME, TO THE CEF-10/CYR61/CTFG/ETSP-12/NOV PROTEIN				
CC	FAMILY.				
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
CC	CC				
DR	EMBL: U09808; AAC24234.1; -				
DR	FLYBASE: FBgn003865; tsg.				
KW	Developmental protein; signal.				
FT	STGNL				
FT	CHAIN				
FT	CARBOHYD				
FT	SEQUENCE				
FT	249 AA; 27220 MW; 313566406E4B86D CRC64;				
Query Match	30.98; Score 537; DB 1; Length 249;				
Best Local Similarity	35.48; Pred. No. 4.07e-100;				
Matches	79; Conservative				
	54; Mismatches 71; Indels 19; Gaps 13;				

DB 1 MOLCYFVILFVGIAPW-SSLANDGNEVYSGVSKLITQSCCKRLND--CHCKRC 57  
 QY 1 MKLH-YVAVLTLLMLFLWLPSPSLSCNALKASDVSKCLIDELCCRCRGENSCCKRC 59  
 DB 58 LNCGLYELTCCGCLDMC-PKHANDVLPSTLRSEIGDI-EGVPELFDLTAEDE-GMST 114  
 QY 60 MCLGALMDECCDVGMCNPNRNSDTPP-TSKSTVELEHPIPSLFALTEGDTQLNMNI 118  
 DB 115 IIRSMAGFOR---V---QG-GAS--GDAGNGNGNNG-SAGVT-LCTVIYVNSCIRA 163  
 QY 119 VSPFAEELSHENLVFLETYNQPHOVYVPSNNVHAPYSSDXKHMCTVYFDDCKSI 178  
 DB 164 NKCRQCESGASSYRFHDGCECEGENCLNNGINESCRGC 206  
 QY 179 HCKICSESGASKYRPFHFNACCCECIGPECIDIGSKTYACMNC 221

RESULT 2  
 ID ITB7\_HUMAN STANDARD: PRT: 798 AA.  
 AC P26010:  
 01-MAY-1992 (Rel. 22, Created)  
 01-MAY-1992 (Rel. 22, Last sequence update)  
 15-FEB-2000 (Rel. 39, Last annotation update)  
 DI INTEGRIN BETA-7 PRECURSOR.  
 GN ITGB7.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 NC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-LEUKOCYTE;  
 RX MEDLINE: 91250405.  
 RA Erie D.J., Ruessig C., Sheppard D., Pytela R.;  
 RT "Complete amino acid sequence of an integrin beta subunit (beta 7)  
 identified in leukocytes."  
 RL J. Biol. Chem. 266:1109-11016(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 91190778.  
 RA Yuan Q., Jiang W.-M., Kissansen G.W., Watson J.D.;  
 RT "Cloning and sequence analysis of a novel beta 2-related integrin  
 transcript from T lymphocytes: homology of integrin cysteine-rich  
 repeats to domain II of laminin B chains."  
 RL Int. Immunol. 2:1097-1108(1990).  
 RN [3]  
 RP REVISIONS.  
 RX MEDLINE: 92135083.  
 RA Yuan Q., Jiang W.-M., Kissansen G.W., Watson J.D.;  
 RT "Cloning and sequence analysis of a novel beta 2-related integrin  
 transcript from T lymphocytes: homology of integrin cysteine-rich  
 repeats to domain III of laminin B chains."  
 RL Int. Immunol. 3:1373-1374(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 93002753.  
 RA Jiang W.-M., Jenkins D., Yuan Q., Leung E., Choo K.H., Watson J.D.,  
 RT "The gene organization of the human beta 7 subunit, the common beta  
 subunit of the leukocyte integrins HML-1 and LPAM-1."  
 RL Int. Immunol. 4:1031-1040(1992).  
 CC -1- FUNCTION: EXPECTED TO PLAY A ROLE IN ADHESIVE INTERACTIONS OF  
 CC LEUKOCYTES. INTERACTS WITH ALPHA-4 (TO FORM LPAM-1) OR WITH  
 CC ALPHA-E (TO FORM HML-1).  
 CC -1- SUBUNIT: DIMER OF AN ALPHA AND BETA SUBUNIT. BETA-7 ASSOCIATES  
 CC WITH ALPHA-4 AND -TEL.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF BETA-7 SUBUNIT MAY  
 CC ARISE BY ALTERNATIVE SPLICING OF PRIMARY MNA TRANSCRIPTS.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF LEUKOCYTE LINES.  
 CC -1- PTM: THE CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN DISULFIDE  
 CC BONDS.  
 CC -1- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.

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 CC -----  
 DR EMBL: S80335; AAB21332.1; -;  
 DR EMBL: M62880; AAA59184.1; -;  
 DR EMBL: M68892; AAA59184.1; -;  
 DR EMBL: S49378; AAB23688.1; -;  
 DR EMBL: S49364; AAB23688.1; JOINED.  
 DR EMBL: S49365; AAB23688.1; JOINED.  
 DR EMBL: S49366; AAB23688.1; JOINED.  
 DR EMBL: S49367; AAB23688.1; JOINED.  
 DR EMBL: S49368; AAB23688.1; JOINED.  
 DR EMBL: S49369; AAB23688.1; JOINED.  
 DR EMBL: S49370; AAB23688.1; JOINED.  
 DR EMBL: S49371; AAB23688.1; JOINED.  
 DR EMBL: S49373; AAB23688.1; JOINED.  
 DR EMBL: S49374; AAB23688.1; JOINED.  
 DR EMBL: S49375; AAB23688.1; JOINED.  
 DR EMBL: S49377; AAB23688.1; JOINED.  
 DR EMBL: L23823; AAA36118.1; -;  
 DR EMBL: L23810; AAA36118.1; JOINED.  
 DR EMBL: L23811; AAA36118.1; JOINED.  
 DR EMBL: L23812; AAA36118.1; JOINED.  
 DR EMBL: L23813; AAA36118.1; JOINED.  
 DR EMBL: L23814; AAA36118.1; JOINED.  
 DR EMBL: L23815; AAA36118.1; JOINED.  
 DR EMBL: L23816; AAA36118.1; JOINED.  
 DR EMBL: L23817; AAA36118.1; JOINED.  
 DR EMBL: L23818; AAA36118.1; JOINED.  
 DR EMBL: L23819; AAA36118.1; JOINED.  
 DR EMBL: L23820; AAA36118.1; JOINED.  
 DR EMBL: L23822; AAA36118.1; JOINED.  
 DR PIR: A40526; A40526.  
 DR MIT: 147559; -;  
 DR PFM: PFM0362; Integrin\_B; 1.  
 DR PRINTS: PRO1186; INTEGRIN.  
 DR PROSITE: PS00243; INTEGRIN\_BETA; 3.  
 DR PROSITE: PS00222; EGF\_1; UNKNOWN 4.  
 DR PROSITE: PS01186; EGF\_2; UNKNOWN 1.  
 KW Integrin; Cell adhesion; Transmembrane; Glycoprotein; Repeat;  
 KW Extracellular matrix; Cytoskeleton; Signal; Phosphorylation;  
 KW Alternative splicing.  
 FT SIGNAL 1 19  
 FT CHAIN 20 798  
 FT DOMAIN 20 723  
 FT TRANSMEM 724 746  
 FT DOMAIN 747 798  
 FT DOMAIN 478 640  
 FT REPEAT 478 526  
 FT REPEAT 527 565  
 FT REPEAT 566 604  
 FT REPEAT 605 640  
 FT CARBOHYD 68 68  
 FT CARBOHYD 279 279  
 FT CARBOHYD 434 434  
 FT CARBOHYD 477 477  
 FT CARBOHYD 531 531  
 FT CARBOHYD 590 590  
 FT CARBOHYD 655 655  
 FT MOD\_RES 674 674  
 FT VARSPPLIC 501 648  
 FT SEQUENCE 798 AA; 86903 MW; CBB275E0B9992385 CMC64;  
 Query Match 6.0%; Score 104; DB 1; Length 798;  
 Best Local Similarity 31.6%; Pred. No. 7.22e-03;



Matches 18; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

Db 598 CSGDMDCISPEGGC-SGHGCKNRCQCLDYGALCDQCPCKTPERRHDCAE 653  
 31 CASDVSKCLIQELQCRPRGNCSCCK-ECM-LCLGALMDECCDVGMCNP-RNYS D 84

Query 3  
 ID COX2\_PANDE STANDARD; PRT; 194 AA.  
 AC P08303;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 15-FEB-2000 (Rel. 39, Last annotation update)  
 DE PROBABLE CYTOCHROME C OXIDASE ASSEMBLY PROTEIN (COX LOCUS HYPOTHETICAL PROTEIN 3).  
 OS Paracoccus denitrificans.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;  
 RN Paracoccus.  
 [1]  
 RP SEQUENCE FROM N.A.  
 RA Raitio M., Jalli T., Saraste M.;  
 RT "Isolation and analysis of the genes for cytochrome c oxidase in Paracoccus denitrificans."  
 RL EMBO J. 6:2825-2833(1987).  
 CC -1- FUNCTION: PROBABLE EXTERNS INS EFFECT AT SOME TERMINAL STAGE OF ENZYME SYNTHESIS, PERHAPS IN DIRECTING ASSEMBLY OF THE SUBUNITS (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE COX11 FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: X05828; CAA29271.1; -;  
 DR DR PIR: S03806; S03806.  
 KM Transmembrane.  
 FT TRANSMEM 13 33 POTENTIAL.  
 FT SEQUENCE 194 AA: 21325 MW; 91866FA4F39B0E2 CRC64;  
 SQ

Query Match 5.8%; Score 101; DB 1; Length 194;  
 Best Local Similarity 25.5%; Pred. No. 2,16e-02;  
 Matches 25; Conservative 20; Mismatches 48; Indels 5; Gaps 5;

Db 23 MGALSMANVPFYSCVGTGAGCTTNAEASDVTDEKTRVF-D-ANADSNIGWTFP 80  
 63 LGAL-WDECCDVGMCNPRNSDPTPTSKTVEE-LHEPISLFRALTEGDTOLNMNIVS 120

Db 81 MOREMELKIGENAIIFYEAINNTDEPTGTASYNVV-AP 117  
 121 PPVAELSHENLVSLFETVQPHQNVSVPSNNVHAP 158

RESULT 4  
 ID GTT2\_MOUSE STANDARD; PRT; 243 AA.  
 AC 061133; 061134; 064472;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE GLUTATHIONE S-TRANSFERASE THETA 2 (EC 2.5.1.18) (GST CLASS-THETA).  
 GN GSTT2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-129/SV, AND B6/CBA; TISSUE-LIVER;  
 RX MEDLINE: 96207306.  
 RA Whittington A.T., Webb G.C., Baker R.T., Board P.G.;  
 RT "Characterization of a cDNA and gene encoding the mouse theta class

RT glutathione transferase mGSTT2 and its localization to chromosome 10B5-Cl.",  
 RL Genomics 33:105-111(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-B6C3F1; TISSUE-LIVER, AND LUNG;  
 RX MEDLINE: 96358519.  
 RA Malinwaring G.W., Williams S.M., Foster J.R., Tugwood J., Green T.;  
 RT "The distribution of theta-class glutathione S-transferases in the liver and lung of mouse, rat and human."  
 RL Biochem. J. 318:297-303(1996).  
 CC -1- FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES.  
 CC -1- CATALYTIC ACTIVITY: RX + GLUTATHIONE -> HX + R-S-GUTATHIONE.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR.  
 CC -1- TISSUE SPECIFICITY: IN LIVER, HIGHEST EXPRESSION FOUND IN CENTRAL VEIN LIMITING PLATE HEPATOCYTES. ALSO EXPRESSED IN INTERLOBULAR BILE DUCT EPITHELIAL CELLS. IN LUNG, EXPRESSED IN CLARA CELLS AND CLILATED CELLS OF THE BRONCHIOALAR EPITHELIUM AND IN TYPE II ALVEOLAR CELLS OF THE LUNG PARENCHYMA.  
 CC -1- SIMILARITY: BELONGS TO THE GST SUPERFAMILY, THETA FAMILY.  
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 CC -----  
 CC EMBL: U48419; AAB03533.1; -;  
 DR EMBL: U48420; AAB03534.1; -;  
 DR EMBL: X98056; CAA66666.1; -;  
 DR MGD: MGI:106188; GSTT2.  
 DR PFM: PF00043; GST. 1.  
 KM Transferase; Multigene family; Nuclear protein.  
 FT INIT\_MET 0 0 BY SIMILARITY.  
 FT VARIANT 37 37 MISSING (IN STRAIN 129/SV).  
 FT VARIANT 66 66 S -> R (IN STRAIN 129/SV).  
 FT VARIANT 177 177 G -> A (IN STRAINS 129/SV AND B6C3F1).  
 FT VARIANT 205 205 Y -> C (IN STRAINS 129/SV AND B6C3F1).  
 SQ SEQUENCE 243 AA: 27549 MW; AC97D35B59342726 CRC64;

Query Match 5.6%; Score 97; DB 1; Length 243;  
 Best Local Similarity 32.9%; Pred. No. 8.98e-02;  
 Matches 23; Conservative 19; Mismatches 22; Indels 6; Gaps 6;

Db 168 STEELMOPV-GIGYULFEGRPOLIMRERVEAF-LGAE-L-YQEAHSTLILGQAAKML 224  
 92 TVEELHEPISLFRALTEGDTOLN-W-NIV-SFVAELSHENLVSLFETVQPHQNV 148

Db 225 PVPPEVHAS 234  
 149 SVPSNNVHAP 158

RESULT 5  
 ID ITB7\_MOUSE STANDARD; PRT; 806 AA.  
 AC P26011; 064656;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (4290 IEL ANTIGEN).  
 GN ITGB7.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 92390425.  
 RA Hu M.C.T., Crowe D.T., Weissman I.L., Holzman B.;  
 RT "Cloning and expression of mouse Integrin beta p(beta 7): a

functional role in Peyer's patch-specific lymphocyte homing.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 89:8254-8258(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 92218384.  
 RA Yuan Q., Jiang W.-M., Leung E., Hollander D., Watson J.D.,  
 RT RT Kriksansen G.W.;  
 RL "Molecular cloning of the mouse integrin beta 7 subunit.";  
 RN J. Biol. Chem. 267:7352-7358(1992).  
 RP [3]  
 RX SEQUENCE FROM N.A.  
 RX MEDLINE: 92388664.  
 RA Gurish M.F., Bell A.F., Smith T.J., Ducharme L.A., Wang R.K.,  
 RT RT Weiss J.H.;  
 RL "Expression of murine beta 7, alpha 4, and beta 1 integrin genes by  
 J. Immunol. 149:1964-1972(1992).  
 RN [4]  
 RP SEQUENCE OF 1-90 FROM N.A., AND SEQUENCE OF 20-32.  
 RX MEDLINE: 91248239.  
 RA Yuan Q., Jiang W.-M., Hollander D., Leung E., Watson J.D.,  
 RT RT Kriksansen G.W.;  
 RL "Identity between the novel integrin beta 7 subunit and an antigen  
 found highly expressed on intraepithelial lymphocytes in the small  
 intestine.";  
 RN Biochem. Biophys. Res. Commun. 176:1443-1449(1991).  
 RP [5]  
 RX SEQUENCE OF 1-67 FROM N.A.  
 RX MEDLINE: 93305607.  
 RA Leung E., Mead P.E., Yuan Q., Jiang W.M., Watson J.D.,  
 RT RT Kriksansen G.W.;  
 RL "The mouse beta 7 integrin gene promoter: transcriptional regulation  
 of the leukocyte integrins LfAM-1 and M290.";  
 RN Int. Immunol. 5:551-558(1993)  
 CC -1- FUNCTION: A COMPONENT OF THE PEYER'S PATCHES-SPECIFIC HOMING  
 RECEPTOR AND IS INVOLVED IN ADHESIVE INTERACTIONS OF LEUKOCYTES.  
 CC -1- SUBUNIT: DIMER OF AN ALPHA AND BETA SUBUNIT. BETA-7 ASSOCIATES  
 WITH ALPHA-4 AND -1EL.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- PM: THE CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN DISULFIDE  
 BONDS.  
 CC -1- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: M68903: AAA02749.1: -;  
 DR EMBL: M95632: AAA39323.1: -;  
 DR EMBL: M95633: AAA39324.1: -;  
 DR EMBL: S44607: AAB23193.1: -;  
 DR EMBL: S63504: AAB27396.1: -;  
 DR PIR: PNO017: PNO017.  
 DR PIR: A46271: A46271.  
 DR PIR: A42483: A42483.  
 DR HSSP: P00750: 1TPG.  
 DR MGI: MGI:96616; 1TPG.  
 DR PFAM: PF00362; Integrin\_B; 1.  
 DR PRINTS: PR01186; INTEGRIN.  
 DR PROSITE: PS00243; INTEGRIN.BETA; 3.  
 DR PROSITE: PS00022; EGF\_1; UNKNOWN\_4.  
 DR PROSITE: PS01186; EGF\_2; UNKNOWN\_1.  
 DR Integrin; Cell adhesion; Transmembrane; Glycoprotein; Repeat;  
 RW Extracellular matrix; Cytoskeleton; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 806 INTEGRIN BETA-7.  
 FT DOMAIN 20 724 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 725 745 POTENTIAL.  
 FT CYTOPLASM 746 806 CYTOPLASMIC (POTENTIAL).  
 FT

FT DOMAIN 478 640 CYSTEINE-RICH REPEATS.  
 FT REPEAT 478 526 I.  
 FT REPEAT 527 565 II.  
 FT REPEAT 566 604 III.  
 FT REPEAT 605 640 IV.  
 FT CARBOHYD 68 68 POTENTIAL.  
 FT CARBOHYD 250 250 POTENTIAL.  
 FT CARBOHYD 279 279 POTENTIAL.  
 FT CARBOHYD 434 434 POTENTIAL.  
 FT CARBOHYD 531 531 POTENTIAL.  
 FT CARBOHYD 590 590 POTENTIAL.  
 FT CARBOHYD 665 665 POTENTIAL.  
 FT CARBOHYD 674 674 POTENTIAL.  
 FT CONFLICT 81 81 A -> E (IN REF. 4).  
 FT CONFLICT 81 81 A -> G (IN REF. 3).  
 FT CONFLICT 124 124 MISSING (IN REF. 2).  
 FT CONFLICT 538 538 S -> C (IN REF. 3).  
 FT CONFLICT 557 557 R -> H (IN REF. 2).  
 SQ SEQUENCE 806 AA; 87411 MW; E793A3F3BA05C18 CRC64;  
 Db 598 CSKSVDSVSPGGILC-SGHGYCKNRCCCLDGYGALCDLGGCKSPCEQYRDAE 653  
 QY 31 CASDVSKCLQLQLCQCPGEGNCSCK-ECW-LCLGALMDECCDVGKCNP-RNTSD 84  
 Query Match 5.6%; Score 97; DB 1; Length 806;  
 Best Local Similarity 31.6%; Pred. No. 8,98e-02;  
 Matches 18; Conservative 12; Mismatches 23; Indels 4; Gaps 4;  
 ID LMB2\_MOUSE STANDARD: PRT: 1799 AA.  
 AC 061292; 062182;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE LAMININ BETA-2 CHAIN PRECURSOR.  
 OS LAMB2 OR S-LAM OR LAMS.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-129/J;  
 RX MEDLINE: 96278760.  
 RA Durkin M.E., Gautam M., Joehel S., Sanes J.R., Nerlie J.P.,  
 RT RT Albrechtsen R., Wewer U.M.;  
 RL "Structural organization of the human and mouse laminin beta2 chain  
 genes, and alternative splicing at the 5' end of the human  
 transcript.";  
 RN J. Biol. Chem. 271:13407-13416(1996).  
 RN [2]  
 RP SEQUENCE OF 348-428 FROM N.A.  
 RC TISSUE-LUNG;  
 RX MEDLINE: 94319092.  
 RA Aberdam D., Galliano M.F., Mattei M.-G., Ortonne J.P., Meneguzzi G.,  
 RT RT "S-laminin gene (lams) maps to F1 band of mouse chromosome 9.";  
 RL Mamm. Genome 5:393-394(1994).  
 RN [3]  
 RP FUNCTION.  
 RC STRAIN-129/J;  
 RX MEDLINE: 95191650.  
 RA Noakes P.G., Gautam M., Mudd J., Sanes J.R., Nerlie J.P.;  
 RT RT "Aberrant differentiation of neuromuscular junctions in mice lacking  
 s-laminin/laminin beta 2.";  
 RL Nature 374:258-262(1995).  
 CC -1- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ  
 IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF  
 CC CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING  
 CC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.  
 CC -1- FUNCTION: LAMININ-3 (S-LAMININ) REGULATES THE FORMATION OF MOTOR  
 CC NERVE TERMINALS.  
 CC -1- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE  
 CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND

CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE  
 CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.  
 CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4  
 CC (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).  
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT  
 CC MEMBRANES (MAJOR COMPONENT).  
 CC -1- TISSUE SPECIFICITY: NEUROMUSCULAR SYNAPSE AND KIDNEY GLOMERULUS.  
 CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT  
 CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.  
 CC -1- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.  
 CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).  
 CC -1- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.  
 CC -----  
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 CC EMBL: U42624; AAC53535.1; JOINED.  
 CC EMBL: X75928; CAA53532.1; -  
 CC HSSP: P02468; IKLO.  
 CC MGD: MGI:99916; LAMB2.  
 CC DR PFAM: PF00053; Laminin\_EGF\_13.  
 CC DR PRINTS: PRO0011; EGF\_LAMININ.  
 CC DR PROSITE: PS01186; EGF\_1; 10.  
 CC DR PROSITE: PS01248; LAMININ\_TYPE\_EGF\_12.  
 CC DR Glycoprotein: Assessment membrane: Extracellular matrix; Coiled coil;  
 CC Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
 CC K1 Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
 CC FT SIGNAL 1 35  
 CC FT CHAIN 36 1799 LAMININ BETA-2 CHAIN.  
 CC FT DOMAIN 36 283 LAMININ N-TERMINAL (DOMAIN VII).  
 CC FT DOMAIN 284 555 4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN  
 CC V).  
 CC FT 286 349 LAMININ EGF-LIKE 1.  
 CC FT 350 412 LAMININ EGF-LIKE 2.  
 CC FT 413 472 LAMININ EGF-LIKE 3.  
 CC FT 473 524 LAMININ EGF-LIKE 4.  
 CC FT 525 555 LAMININ EGF-LIKE 5 (INCOMPLETE).  
 CC FT 556 782 LAMININ DOMAIN IV.  
 CC FT 783 1191 8 X LAMININ EGF-LIKE REPEATS (DOMAIN  
 CC III).  
 CC FT 784 831 LAMININ EGF-LIKE 6.  
 CC FT 832 877 LAMININ EGF-LIKE 7.  
 CC FT 878 927 LAMININ EGF-LIKE 8.  
 CC FT 928 986 LAMININ EGF-LIKE 9.  
 CC FT 987 1038 LAMININ EGF-LIKE 10.  
 CC FT 1039 1095 LAMININ EGF-LIKE 11.  
 CC FT 1096 1143 LAMININ EGF-LIKE 12.  
 CC FT 1144 1190 LAMININ EGF-LIKE 13.  
 CC FT 1191 1410 LAMININ II.  
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RN [2] SEQUENCE FROM N.A.
RX RX OLMEHINE: 92268130.
RA RA Olmeh M.E., Ren H., Ostrowski J., Jacobson K., Stiles G.L.;
RT "Cloning, expression, and characterization of the unique bovine A1
RT adenosine receptor. Studies on the ligand binding site by
RT site-directed mutagenesis."
RL J. Biol. Chem. 267:10764-10770(1992).
CC CC -I- FUNCTION: RECEPTOR FOR ADENOSINE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY G PROTEINS WHICH INHIBIT ADENYLYL CYCLASE.
CC CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC CC -----
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CC or send an email to licensesh@isb.slb.ch).
CC CC -----
DB DB EMBL, X63592; AAA45135.1; -.
DB EMBL, M86261; AAA30350.1; -.
DR DR PIR: S22213; S22213.
DR DR PIR: S20390; S20390.
DR DR HSSP: F29274; IMMH.
DR DR GCRRB; GCR_0284; -.
DR DR PFAM: PF00001; 7cml.1; 1.
DR DR PRINTS: PR00237; GPCRHHODPSN.
DR DR PRINTS: PR00424; ADENOSINER.
DR DR PRINTS: PR00542; ADENOSINER.
DR DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.
DR DR KMW Lipo-protein coupled receptor; Transmembrane; Glycoprotein;
KW Lipoprotein; Palmitate.
FT FT DOMAIN 1 10 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 11 33 CYTOPLASMIC (POTENTIAL).
FT FT DOMAIN 34 46 CYTOPLASMIC (POTENTIAL).
FT FT TRANSMEM 47 69 2 (POTENTIAL).
FT FT DOMAIN 70 80 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 81 102 3 (POTENTIAL).
FT FT DOMAIN 103 123 CYTOPLASMIC (POTENTIAL).
FT FT TRANSMEM 124 146 4 (POTENTIAL).
FT FT DOMAIN 147 176 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 177 201 5 (POTENTIAL).
FT FT DOMAIN 202 235 6 (POTENTIAL).
FT FT TRANSMEM 236 259 7 (POTENTIAL).
FT FT DOMAIN 260 267 7 (POTENTIAL).
FT FT TRANSMEM 268 292 8 (POTENTIAL).
FT FT DOMAIN 293 326 9 (POTENTIAL).
FT FT DISULFID 80 169 10 (POTENTIAL).
FT FT CARBOHYD 148 148 11 (POTENTIAL).
FT FT CARBOHYD 159 159 12 (POTENTIAL).
FT FT LIPID 309 309 13 (POTENTIAL).
FT FT CONFLICT 101 101 14 (POTENTIAL).
SO SO SEQUENCE 326 AA; 36597 MM; 1697A5F30A57285 CRC64;

Query Match 5.5%; Score 96; DB 1; Length 326;
Best Local Similarity 37.1%; Pred. No. 1.27e+01;
Matches 13; Conservative 11; Mismatches 8; Indels 3; Gaps 3;

Db Db 236 LALLIEFALSWLPRIHLINCITLFPCSCHEMRILL 270
Qy Qy 9 LTLAIIMF-LTWLP-ESISCNKALCAS-DVSKCII 40

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[illegible]

CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE: 90260639.  
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,  
 RA Dover S.K., Cosman D., Goodwin R.G.;  
 RT "A receptor for tumor necrosis factor defines an unusual family of  
 RT cellular and viral proteins.";  
 RL Science 248:1019-1023(1990).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE: 91045991.  
 RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,  
 RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;  
 RT "A second tumor necrosis factor receptor gene product can shed a  
 RT naturally occurring tumor necrosis factor inhibitor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE: 96299745.  
 RA Bellinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,  
 RA Lepassier D., Stallard B.J., Goeddel D.V., Desauvage F.J.;  
 RA Brodeur G.M.;  
 RT "Physical mapping and genomic structure of the human TNFR2 gene.";  
 RL Genomics 35:94-100(1996).  
 RN [4]  
 RN SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE: 90349572.  
 RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,  
 RA Ringold G.M.;  
 RT "Complementary DNA cloning of a receptor for tumor necrosis factor  
 RT and demonstration of a shed form of the receptor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).  
 RN [5]  
 RN SEQUENCE OF 27-31.  
 RX MEDLINE: 90110215.  
 RA Engelmann H., Novick D., Wallach D.;  
 RT "Two tumor necrosis factor-binding proteins purified from human  
 RT urine. Evidence for immunological cross-reactivity with cell surface  
 RT tumor necrosis factor receptors.";  
 RL J. Biol. Chem. 265:1531-1536(1990).  
 RN [6]  
 RN SEQUENCE OF 22-40; 65-69; 136-141; 300-306 AND 346-362.  
 RX MEDLINE: 91056048.  
 RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,  
 RA Brockhaus M.;  
 RT "Purification and partial amino acid sequence analysis of two  
 RT distinct tumor necrosis factor receptors from HL60 cells.";  
 RL J. Biol. Chem. 265:20131-20138(1990).  
 RN [7]  
 RN CHARACTERIZATION.  
 RX MEDLINE: 93016040.  
 RA Penica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,  
 RA Lipari M.T., Goeddel D.V.;  
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.  
 RT Characterization of ligand binding, internalization, and receptor  
 RT phosphorylation.";  
 RL J. Biol. Chem. 267:21172-21178(1992).  
 RN [8]  
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX.  
 RX MEDLINE: 99221490.  
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;  
 RT "Structural basis for self-association and receptor recognition of  
 RT human TRAF2.";  
 RL Nature 398:533-538(1999).  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND  
 CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW  
 CC LEVEL ON THREONINE RESIDUES.  
 CC -1- PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND  
 CC WYETH-AVENTIS). USED TO TREAT MODERATE TO SEVERE RHEUMATOID  
 CC ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING

CC PORTION OF TNFR2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO  
 CC TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm".  
 CC -1- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;  
 CC WWW="http://www.enbrelinfo.com/".  
 CC -----  
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 CC -----  
 DR EMBL: M3315; AAA59929.1; -  
 DR EMBL: M35857; AAA63262.1; -  
 DR EMBL: U52165; AAC50622.1; JOINED.  
 DR EMBL: U52156; AAC50622.1; JOINED.  
 DR EMBL: U52157; AAC50622.1; JOINED.  
 DR EMBL: U52158; AAC50622.1; JOINED.  
 DR EMBL: U52159; AAC50622.1; JOINED.  
 DR EMBL: U52160; AAC50622.1; JOINED.  
 DR EMBL: U52161; AAC50622.1; JOINED.  
 DR EMBL: U52162; AAC50622.1; JOINED.  
 DR EMBL: U52163; AAC50622.1; JOINED.  
 DR EMBL: U52164; AAC50622.1; JOINED.  
 DR EMBL: M55994; AAA36755.1; -  
 DR PIR: A35356; A35356.  
 DR PIR: A36007; A36007.  
 DR PIR: A36475; A36475.  
 DR PIR: B35010; B35010.  
 DR PIR: A23666; A23666.  
 DR PDB: 1CA9; 12-APR-99.  
 DR MTM: 191191; -  
 DR PRAM: PF00020; TNFR\_C6; 4.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 4.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;  
 KW Phosphorylation; Pharmaceutical; 3D-structure.  
 FT SIGNAL 1 22  
 FT CHAIN 23 461  
 FT DOMAIN 23 257  
 FT TRANSMEM 258 287  
 FT DOMAIN 288 461  
 FT REPEAT 39 201  
 FT REPEAT 39 201  
 FT REPEAT 77 118  
 FT REPEAT 119 162  
 FT REPEAT 163 201  
 FT DISULFID 40 53  
 FT DISULFID 54 67  
 FT DISULFID 57 75  
 FT DISULFID 78 93  
 FT DISULFID 96 110  
 FT DISULFID 100 118  
 FT DISULFID 120 126  
 FT DISULFID 134 143  
 FT DISULFID 137 161  
 FT DISULFID 161 179  
 FT CARBOHYD 171 171  
 FT CARBOHYD 193 193  
 FT CARBOHYD 141 141  
 FT CONFLICT 196 196  
 FT CONFLICT 363 363  
 SQ SEQUENCE 461 AA; 48316 MW; 603B580EC67636F CRC64;  
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 Best Local Similarity 42.4%; Pred. No. 1.80e-01;  
 Matches 25; Conservative 10; Mismatches 13; Indels 11; Gaps 11;  
 Db 89 WPECLSCG-SRCSDDVETOACTREONRICICRPG-WICALSKOBGCRIC-APLRK-C 143



Query Match	Similarity	Score	DB	Length
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Matches 11; Conservative	7;	Fred. No. 1.27e-01;		
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	Indels 0;			
	Gaps 0;			

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE: 89034134.  
RA Sasaki M., Kleinman H.K., Huber H., Deutzmann R., Yamada Y.;  
RT "Laminin, a multidomain protein. The A chain has a unique globular  
RT domain and homology with the basement membrane proteoglycan and the  
RT laminin B chains";  
RL J. Biol. Chem. 263:16536-16544(1988).  
RN [2]  
RP SEQUENCE OF 1-339 FROM N.A.  
RX MEDLINE: 88225080.  
RA Hartl L., Oberhaeumer I., Deutzmann R.;  
RT "The N terminus of laminin A chain is homologous to the B chains.";  
RL Eur. J. Biochem. 173:629-635(1988).  
RN [3]  
RP SEQUENCE OF 2538-3084 FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE: 89030693.  
RA Deutzmann R., Huber J., Schmetz K.A., Oberhaeumer I., Hartl L.;  
RT "Structural study of long arm fragments of laminin. Evidence for  
RT repetitive C-terminal sequences in the A-chain, not present in the B-  
RT chains";  
RL Eur. J. Biochem. 177:35-45(1988).  
RN [4]  
CC -1- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ  
CC IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF  
CC CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING  
CC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.  
CC -1- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE  
CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND  
CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE  
CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.  
CC THE ALPHA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ) AND  
CC LAMININ-3 (S-LAMININ).  
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
CC -1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR  
CC COMPONENT).  
CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT  
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.  
CC -1- DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.  
CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).  
CC -1- SIMILARITY: CONTAINS 17 LAMININ G-LIKE DOMAINS.  
CC -1- SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.  
CC -1- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.  
CC  
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CC -----  
DR EMBL: J04064; AAA39410.1; -  
DR EMBL: X07737; CAA30561.1; -  
DR EMBL: X13459; CAA31807.1; -  
DR EMBL: M36775; AAA39406.1; -  
DR PIR: A31771; MMSA.  
DR HSSP: P02468; TITLE.  
DR MGD: MGI:98892; LAM1.  
DR PFAM: PF00052; laminin\_B; 2.  
DR PFAM: PF00053; laminin\_Egf; 15.  
DR PFAM: PF00054; laminin\_G; 5.  
DR PFAM: PF00055; laminin\_Nterm; 1.  
DR PRINTS: PR00011; EGF/LAMININ.  
DR PROSITE: PS00022; EGF\_1; 11.  
DR PROSITE: PS01186; EGF\_2; 3.  
DR PROSITE: PS01248; LAMININ\_TYPE\_EGF; 15.  
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
KW Laminin Egf-like domain; Cell adhesion; Repeat; Signal.  
FT SIGNAL 1 24 POTENTIAL.  
FT CHAIN 25 3084 LAMININ ALPHA-1 CHAIN.  
FT MOD RES 25 256 BLOCKED.  
FT DOMAIN 25 276 LAMININ N-TERMINAL (DOMAIN VI).  
FT DOMAIN 277 519 4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN  
V).

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FT DOMAIN 277 333 LAMININ EGF-LIKE 1.
FT DOMAIN 334 403 LAMININ EGF-LIKE 2.
FT DOMAIN 404 460 LAMININ EGF-LIKE 3.
FT DOMAIN 461 509 LAMININ EGF-LIKE 4.
FT DOMAIN 510 519 LAMININ EGF-LIKE 5 (N-TERMINAL).
FT DOMAIN 520 715 LAMININ DOMAIN IV 1 (DOMAIN IV B).
FT DOMAIN 716 1166 9 X LAMININ EGF-LIKE REPEATS (DOMAIN
III B).
FT DOMAIN 716 748 LAMININ EGF-LIKE 5 (C-TERMINAL).
FT DOMAIN 749 797 LAMININ EGF-LIKE 6.
FT DOMAIN 798 855 LAMININ EGF-LIKE 7.
FT DOMAIN 856 908 LAMININ EGF-LIKE 8.
FT DOMAIN 909 957 LAMININ EGF-LIKE 9.
FT DOMAIN 958 1004 LAMININ EGF-LIKE 10.
FT DOMAIN 1005 1050 LAMININ EGF-LIKE 11.
FT DOMAIN 1051 1096 LAMININ EGF-LIKE 12.
FT DOMAIN 1097 1156 LAMININ EGF-LIKE 13.
FT DOMAIN 1157 1166 LAMININ EGF-LIKE 14 (N-TERMINAL).
FT DOMAIN 1167 1368 LAMININ DOMAIN IV 2 (DOMAIN IV A).
FT DOMAIN 1369 1561 3.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
III A).
FT DOMAIN 1369 1409 LAMININ EGF-LIKE 14 (C-TERMINAL).
FT DOMAIN 1410 1458 LAMININ EGF-LIKE 15.
FT DOMAIN 1459 1515 LAMININ EGF-LIKE 16.
FT DOMAIN 1516 1562 LAMININ EGF-LIKE 17.
FT DOMAIN 1562 2133 DOMAIN II AND I.
FT DOMAIN 2134 3084 5 X LAMININ G-LIKE REPEATS (DOMAIN G).
FT DOMAIN 2148 2335 LAMININ G-LIKE 1.
FT DOMAIN 2336 2517 LAMININ G-LIKE 2.
FT DOMAIN 2518 2745 LAMININ G-LIKE 3.
FT DOMAIN 2746 2922 LAMININ G-LIKE 4.
FT DOMAIN 2923 3084 LAMININ G-LIKE 5.
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FT DOMAIN 1869 1903 COILED COIL (POTENTIAL).
FT DOMAIN 2096 2128 COILED COIL (POTENTIAL).
FT DOMAIN 1147 1149 CELL ATTACHMENT SITE.
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FT DISULFID 1549 1560 BY SIMILARITY.
FT DISULFID 1563 1563 INTERCHAIN (PROBABLE).
FT DISULFID 1567 1567 INTERCHAIN (PROBABLE).
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FT CARBOHYD 770 770 POTENTIAL.
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FT CARBOHYD 914 914 POTENTIAL.
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FT CARBOHYD 1052 1052 POTENTIAL.
FT CARBOHYD 1344 1344 POTENTIAL.
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FT CARBOHYD 1603 1603 POTENTIAL.
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FT CARBOHYD 1686 1686 POTENTIAL.
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FT CARBOHYD 1718 1718 POTENTIAL.
FT CARBOHYD 1725 1725 POTENTIAL.

Note: remainder of annotations omitted.

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Best Local Similarity 37.5%; Pred. No. 1,27e+01;
Matches 15; Conservative 6; Mismatches 17; Indels 2; Gaps 2;

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RESULT 13
ID WT_XENLA STANDARD; PRT; 62 AA.
AC 005890;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN.
GN MT-A.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE; 93263990.
RA St Jacques E., Seguin C.;
RT "Cloning and nucleotide sequence of a complementary DNA encoding

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FT DISULFID 1556 1556 INTERCHAIN (PROBABLE).
FT DISULFID 1560 1560 INTERCHAIN (PROBABLE).
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FT CARBOHYD 555 555 POTENTIAL.
FT CARBOHYD 665 665 POTENTIAL.
FT CARBOHYD 763 763 POTENTIAL.
FT CARBOHYD 926 926 POTENTIAL.
FT CARBOHYD 952 952 POTENTIAL.
FT CARBOHYD 1045 1045 POTENTIAL.
FT CARBOHYD 1407 1407 POTENTIAL.
FT CARBOHYD 1579 1579 POTENTIAL.
FT CARBOHYD 1596 1596 POTENTIAL.
FT CARBOHYD 1678 1678 POTENTIAL.
FT CARBOHYD 1689 1689 POTENTIAL.
FT CARBOHYD 1698 1698 POTENTIAL.
FT CARBOHYD 1717 1717 POTENTIAL.
FT CARBOHYD 1804 1804 POTENTIAL.
FT CARBOHYD 1894 1894 POTENTIAL.
FT CARBOHYD 1898 1898 POTENTIAL.
FT CARBOHYD 1957 1957 POTENTIAL.
FT CARBOHYD 1974 1974 POTENTIAL.
FT CARBOHYD 1991 1991 POTENTIAL.
FT CARBOHYD 2038 2038 POTENTIAL.
FT CARBOHYD 2047 2047 POTENTIAL.
FT CARBOHYD 2094 2094 POTENTIAL.
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Note: remainder of annotations omitted.

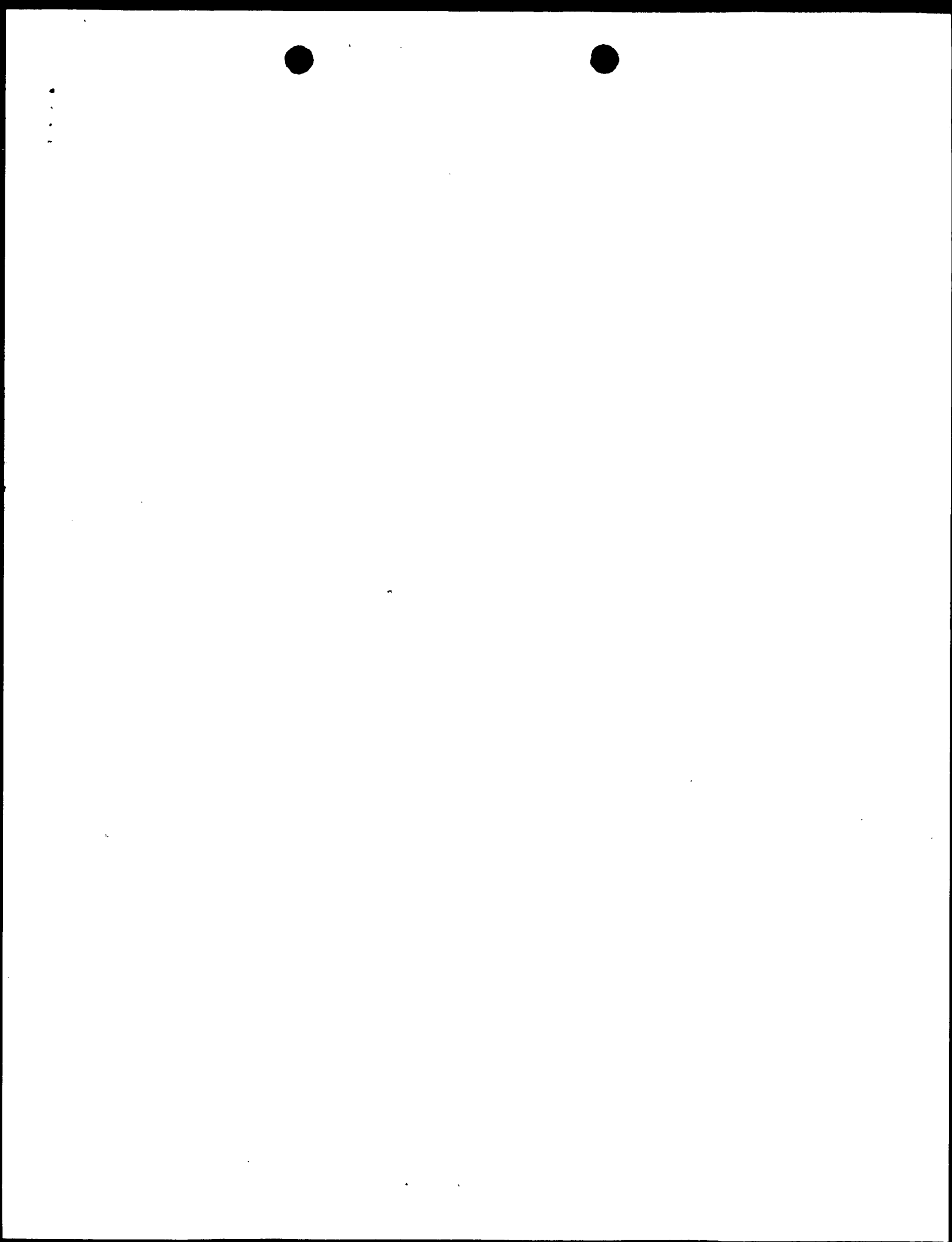
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Best Local Similarity 5.4%; Score 94; DB 1; Length 3075;

Matches 14; Conservative 8; Mismatches 16; Indels 2; Gaps 2;

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QY 20 LPESLSCNKALCASDVSKC-LIGELCQCRPGEGNCSCKE 58

Search completed: Wed Aug 16 09:32:22 2000  
Job time : 42 secs.





179 HOCKISCESMGASKYRFRFNACCECTPECIDYGSKIVKCMNC 221

RESULT 2

ENTRY A40526 #type complete

TITLE integrin beta-7 chain precursor - human

ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change

20-Aug-1999

ACCESSIONS A40526; A43979; A49825; I54746; I54749

REFERENCE A40526

#authors Erle, D.J.; Rueegg, C.; Sheppard, D.; Pytela, R.

#journal J. Biol. Chem. (1991) 266:11009-11016

#title Complete amino acid sequence of an integrin beta subunit (beta-7) identified in leukocytes.

#cross-references M01D:91250405

#accession A40526

#molecule-type mRNA

#residues 1-798 ##label ERL

#cross-references GB:M62880; NID:g186510; PIDN:AAA59185.1; PID:g186511

REFERENCE A43979

#authors Yuan, Q.; Jiang, W.M.; Krissansen, G.W.; Watson, J.D.

#journal Int. Immunol. (1990) 2:1097-1108

#title Cloning and sequence analysis of a novel beta-2-related integrin transcript from T lymphocytes: homology of integrin cysteine-rich repeats to domain III of laminin B chains

#cross-references M01D:91190778

#accession A43979

#molecule-type mRNA

#residues 1-133, 'R', '135-161', 'S', '163-309', 'S', '311-490', 'A', '493-505', 'A', '507-571', 'W', '573-707', 'A', '709-730', 'W', '732-798' ##label YUA

#cross-references GB:M68892

REFERENCE A49825

#authors Micklem, K.D.; Dong, Y.; Willis, A.; Pullford, K.A.; Visser, L.; Durkop, H.; Poppeema, S.; Stein, H.; Mason, D.Y.

#journal Am. J. Pathol. (1991) 139:1297-1301

#title HML-1 antigen on mucosa-associated T cells, activated cells, and hairy leukemic cells is a new integrin containing the beta 7 subunit.

#cross-references M01D:92087874

#accession A49825

#molecule-type protein

#residues 20-21, 'X', '23-31', 'X', '33', 'A' ##label MTC

#experimental\_source spleen, hairy cell membranes

#note sequence extracted from NCBI backbone (NCBIP:71419)

REFERENCE I54746

#authors Yuan, Q.A.; Jiang, W.M.; Krissansen, G.W.; Watson, J.D.

#journal Int. Immunol. (1991) 3:1373-1374

#title Cloning and sequence analysis of a novel beta 2-related integrin cysteine-rich repeats to domain III of laminin B chains

#cross-references M01D:92135083

#accession I54746

#molecule-type mRNA

#residues 1-798 ##label RES

#cross-references GB:S60335; NID:g244680; PIDN:AAB21332.1; PID:g244681

REFERENCE I54749

#authors Jiang, W.M.; Jenkins, D.; Yuan, Q.; Leung, E.; Choo, K.H.; Watson, J.D.; Krissansen, G.W.

#journal Int. Immunol. (1992) 4:1031-1040

#title The gene organization of the human beta 7 subunit, the common beta subunit of the leukocyte integrins HML-1 and LfPM-1.

#cross-references M01D:93002753

#accession I54749

#molecule-type DNA

#status preliminary; translated from GB/EMBL/DBJ

#cross-references GB:S49378; NID:g257583; PIDN:AAB23688.1; PID:g257584

GENETICS GDB:ITGB7

#gene

#cross-references GDB:128601; OMIM:147559

#map\_position 12q13.13-12q13.13

#introns 67/3; 135/1; 192/1; 272/3; 325/3; 357/3; 387/3; 436/3; 501/2; 576/1; 649/2; 719/1; 772/3

CLASSIFICATION #superfamily integrin beta chain; laminin-type EGF-like homology

KEYWORDS alternative splicing; cell adhesion; cytoskeleton; duplication; heterodimer; phosphoprotein; transmembrane protein

FEATURE 20-798

726-746

SUMMARY #product integrin beta-7 chain #status experimental

#label MAT

#domain transmembrane #status predicted #label TMM

#length 798 #molecular-weight 86902 #checksum 6264

Query Match 6.0%; Score 104; DB 2; Length 798;

Best Local Similarity 31.6%; Pred. No. 4.19e-02;

Matches 18; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

DB 598 CSGDMSGISPEGLC-SGGRCKNRCQCIDGYGALCDQCPGCKTPERRHDCAE 653

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31 CASDVSCKLIQLQLQCRPGSGNCSCK-ECM-LCLGLNDECCDCVGMCP-RNYSD 84

RESULT 3

ENTRY T01616 #type complete

TITLE hypothetical protein F19F24.8 - Arabidopsis thaliana

ORGANISM #formal\_name Arabidopsis thaliana #common\_name mouse-ear cress

DATE 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change

14-May-1999

ACCESSIONS T01616

REFERENCE Z14153

#authors Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul, S.; Mason, T.M.; Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter, J.C.

#submission submitted to the EMBL Data Library, April 1998

#description Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence.

#accession T01616

#status translated from GB/EMBL/DBJ

#molecule-type DNA

#residues 1-417 ##label ROU

#cross-references EMBL:AC003673; NID:g3004543; PID:g3004551

#experimental\_source cultivar Columbia

GENETICS

#map\_position 2

#introns 103/3; 200/1

F19F24.8

SUMMARY #length 417 #molecular-weight 47606 #checksum 1252

Query Match 5.9%; Score 102; DB 2; Length 417;

Best Local Similarity 27.5%; Pred. No. 8.05e-02;

Matches 22; Conservative 20; Mismatches 34; Indels 4; Gaps 4;

DB 273 WFKIVSFGVEELSHVDEFLYS-ITKLQDEVAVALMNSNKNANKMEKSGSCFG-FEE 330

116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

116 W-NIVSFPVAEELSHENLVSEFLTYNQHONVSPNNHAPYSSDKHEMCTVYFDD 174

DB 331 CAVNLR-QLECSGOVAFSDF 349

116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771

ACCESSIONS S03806  
REFERENCE S03803  
#authors Raitio, M.; Jalli, T.; Saraste, M.  
#journal EMBO J. (1987) 6:2825-2833  
#title Isolation and analysis of the genes for cytochrome c oxidase in *Paracoccus denitrificans*.  
#accession S03806  
#molecule-type DNA  
#residues 1-194 #label RAI  
#cross-references EMBL:X05828; NID:945468; PIDN:CAA29271.1; PID:945472  
CLASSIFICATION #superfamily cytochrome-c oxidase assembly protein COX11  
SUMMARY #length 194 #molecular-weight 21325 #checksum 9149

Query Match 5.8%; Score 101; DB 2; Length 194;  
Best Local Similarity 25.5%; Pred. No. 1.11e-01;  
Matches 25; Conservative 20; Mismatches 48; Indels 5; Gaps 5;

Db 81 MOREMELKIGENAIAPFEAINNTDEPTGTASYNV-AP 117  
QY 121 FVAEELSHENLVSELETYNQPHQNVSPNNVHAP 158

RESULT 5  
ENTRY T08724 #type complete  
TITLE hypothetical protein DKFZ566D213.1 - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 13-Aug-1999  
T08724  
ACCESSIONS T08724  
REFERENCE 216468  
#authors Kohrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
#submission submitted to the Protein Sequence Database, May 1999  
#accession T08724  
#molecule-type mRNA  
#residues 1-417 #label KOE  
#cross-references EMBL:AL050275  
#experimental\_source fetal kidney; clone DKFZ566D213

GENETICS  
#note DKFZ566D213.1  
SUMMARY #length 417 #molecular-weight 44934 #checksum 2694

Very Match 5.8%; Score 100; DB 2; Length 417;  
Best Local Similarity 28.6%; Pred. No. 1.54e-01;  
Matches 14; Conservative 12; Mismatches 21; Indels 2; Gaps 2;

Db 236 WALHLKACVIDECGTGANGADQFCVNTGSECDCAKALGCMGA 284  
QY 19 WLPESLSC-NKALCASDVSQCLQELCQCRPREGNC-SCKECKMLCLGA 65

RESULT 6  
ENTRY S71879 #type complete  
TITLE glutathione transferase (EC 2.5.1.18) theta 2, hepatic - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 21-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 18-Jun-1999  
S71879  
ACCESSIONS S71879  
REFERENCE S71878  
#authors Maitwaring, G.W.; Williams, S.M.; Foster, J.R.; Tugwood, J.; Biochem. J. (1996) 318:297-303  
#journal The distribution of Theta-class glutathione S-transferases in the liver and lung of mouse, rat and human.  
#cross-references MUID:96358519  
#accession S71879  
#status preliminary  
#molecule-type mRNA

#residues 1-244 #label MAI  
#cross-references EMBL:X98056; NID:g1340077; PIDN:CAA66666.1; PID:e245091; PID:g1340078  
#note the authors translated the codon TCA for residue 11 as Ala

CLASSIFICATION #superfamily glutathione transferase  
KEYWORDS transferase  
SUMMARY #length 244 #molecular-weight 27634 #checksum 5537

Query Match 5.6%; Score 97; DB 2; Length 244;  
Best Local Similarity 30.0%; Pred. No. 3.99e-01;  
Matches 21; Conservative 21; Mismatches 22; Indels 6; Gaps 6;

Db 169 SLEELMOPVALGY-NLEGRPOLTAMREYFAF-LGAEICQEAH-STILSLGQAKML 225  
QY 92 TVEELHEPILFLFRALTEGDTQLN-W-NIV-SFVAEELSHENLVSELETYNQPHQNV 148  
Db 226 PVPPEVHAS 235  
QY 149 SVPSNNVHAP 158

RESULT 7  
ENTRY A46271 #type complete  
TITLE integrin beta-7 chain precursor - mouse  
ALTERNATE\_NAMES M290 antigen beta chain  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 21-Sep-1999 #sequence\_revision 18-Nov-1994 #text\_change 20-Aug-1999  
A46271; A42483; B46503; PN0017; A60229  
ACCESSIONS A46271  
REFERENCE A46271  
#authors Hu, M.C.; Crowe, D.T.; Weissman, I.L.; Holzmam, B. Proc. Natl. Acad. Sci. U.S.A. (1992) 89:8254-8258  
#journal Cloning and expression of mouse integrin beta p(beta 7): a functional role in Peyer's patch-specific lymphocyte homing.  
#title  
#cross-references MUID:92390425  
#accession A46271  
#status preliminary  
#molecule-type nucleic acid  
#residues 1-806 #label HUI  
#note sequence extracted from NCBI backbone (NCBIN:113097, NCBIP:113125)

REFERENCE A42483  
#authors Yuan, Q.; Jiang, W.M.; Leung, E.; Hollander, D.; Watson, J.D.; Krissansen, G.W. J. Biol. Chem. (1992) 267:7352-7358  
#journal Molecular cloning of the mouse integrin beta 7 subunit.  
#title  
#cross-references MUID:92218384  
#accession A42483  
#molecule-type mRNA  
#residues 1-123, 125-556, 'H', 558-806 #label YHA  
#cross-references GB:M68903; NID:9349598; PIDN:AAA02749.1; PID:9349599  
#note sequence extracted from NCBI backbone (NCBIN:93455, NCBIP:93463)

REFERENCE A46503  
#authors Gurish, M.F.; Bell, A.F.; Smith, T.J.; Ducharme, L.A.; Wang, R.K.; Weis, J.H. J. Immunol. (1992) 149:1964-1972  
#journal Expression of murine beta 7, alpha 4, and beta 1 integrin genes by rodent mast cells.  
#cross-references MUID:92388664  
#accession B46503  
#status preliminary  
#molecule-type mRNA  
#residues 1-80, 'G', 82-537, 'C', 539-806 #label GUR  
#cross-references GB:S44607; NID:9255138; PIDN:AAB23193.1; PID:9255139  
#experimental\_source spleen  
#note sequence extracted from NCBI backbone (NCBIN:113091, NCBIP:113092)

REFERENCE PN0017  
#authors Yuan, Q.; Jian, W.; Hollander, D.; Leung, E.; Watson, J.D.; Krissansen, G.W.

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#Journal      Biochem. Biophys. Res. Commun. (1991) 176:1443-1449
#title        Identity between the novel integrin beta 7 subunit and an
              antigen found highly expressed on intraepithelial
              lymphocytes in the small intestine.
#cross-references MUID:91248239
#accession    P00017
#status       nucleic acid sequence not shown
#molecule_type mRNA
#residues     1-80, 'E', 82-90 ##label YU2
#authors      Kishaw, P.J.; Murant, S.J.
#journal      Eur. J. Immunol. (1990) 20:2201-2207
#title        A new surface antigen on intraepithelial lymphocytes in the
              intestine.
#cross-references MUID:91055592
#accession    A60229
#status       ##molecule_type protein
              ##residues 20-32 ##label KIT
CLASSIFICATION #superfamily integrin beta chain; laminin-type EGF-like
KEYWORDS       homology
              cell adhesion; cytoskeleton; duplication; extracellular
              matrix; glycoprotein; heterodimer; membrane protein;
              phosphoprotein
FEATURE        1-19
              20-90
              #domain signal sequence #status predicted #label SIG\
              #product integrin beta 7 chain (fragment) #status
              experimental #label IBC
SUMMARY        #length 806 #molecular-weight 87411 #checksum 9972
              5.6% Score 97; DB 2; Length 806;
              Best Local Similarity 31.6%; Pred. No. 3,99e-01;
              Matches 18; Conservative 12; Mismatches 23; Indels 4; Gaps 4;

Db 598 CSKVSVCVSEGGIC-SGHGYCKNCRCQCLDGYGALCDQCLGCKSPCEQRPDCAE 653
OY 31 CASDVSKCLIGELCCCRPGEKSCCK-ECM-LCIGALMDECCOCVGMCMF-RMYSD 84

RESULT 8
ENTRY       A38144 #type complete
TITLE       adenosine receptor A1 - bovine
ORGANISM    #formal_name Bos primigenius taurus #common_name cattle
DATE        04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
              29-Sep-1999
ACCESSIONS  A38144; S20390; S22213
REFERENCE    A38144
#authors     Olah, M.E.; Ren, H.; Ostrowski, J.; Jacobson, K.A.; Stiles,
              G.L.
#journal     J. Biol. Chem. (1992) 267:10764-10770
#title       Cloning, expression, and characterization of the unique
              bovine A1 adenosine receptor. Studies on the ligand binding
              site by site-directed mutagenesis.
#cross-references MUID:92268130
#accession   A38144
#molecule_type mRNA
#residues    1-326 ##label OLA
#cross-references GB:M6261; NID:9162597; PIDN:AAA30350.1; PID:9162598
#experimental_source brain
#note        Sequence extracted from NCBI backbone (NCBIN:103815,
              NCBIP:103816)
REFERENCE    S20390
#authors     Tucker, A.L.; Linden, J.; Robeva, A.S.; D'Angelo, D.D.;
              Lynch, K.R.
#journal     FEBS Lett. (1992) 297:107-111
#title       Cloning and expression of a bovine adenosine A(1):receptor
              cDNA.
#cross-references MUID:92201360
#accession   S20390
#status       ##molecule_type mRNA
              ##residues 1-100, 'W', 102-326 ##label TUC
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              ##experimental_source brain

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CLASSIFICATION #superfamily adenosine receptor A1
KEYWORDS       adenylylate cyclase inhibitor; G protein-coupled receptor;
              glycoprotein; transmembrane protein
FEATURE        148,159
              #binding_site carbohydrate (Asn) (covalent) #status
              predicted
SUMMARY        #length 326 #molecular-weight 36579 #checksum 6464
              5.5% Score 96; DB 2; Length 326;
              Best Local Similarity 37.1%; Pred. No. 5.45e-01;
              Matches 13; Conservative 11; Mismatches 8; Indels 3; Gaps 3;

Db 236 LALILFALSWLPHILNCITFCPSCHMPEIL 270
OY 9 LTLAIIMF-LTWLP-BLSLSCNKLCAAS-DVSKCLI 40

RESULT 9
ENTRY       A42108 #type complete
TITLE       clusterin precursor - pig
ALTERNATE_NAMES complement cytolysis inhibitor; CP40 protein
ORGANISM     #formal_name Sus scrofa domestica #common_name domestic pig
DATE        04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
              13-Aug-1999
ACCESSIONS  A42108; JC5535; PC4475
REFERENCE    A42108
#authors     Diemer, V.; Hoyte, M.; Baglioni, C.; Mills, A.J.
#journal     J. Biol. Chem. (1992) 267:5257-5264
#title       Expression of porcine complement cytolysis inhibitor mRNA in
              cultured aortic smooth muscle cells. Changes during
              differentiation in vitro.
#cross-references MUID:92184774
#accession   A42108
#molecule_type mRNA
#residues    1-446 ##label DIE
#cross-references GB:M84639; NID:9164408; PIDN:AAA31013.1; PID:9164409
#experimental_source aortic smooth muscle cells
#note        sequence extracted from NCBI backbone (NCBIN:87354,
              NCBIP:87356)
REFERENCE    JC5535
#authors     Ogawa, S.; Ishibashi, Y.; Sakamoto, Y.; Kitamura, K.; Kubo,
              M.; Sakai, T.; Inoue, K.
#journal     Biochem. Biophys. Res. Commun. (1997) 234:712-718
#title       The glycoproteins that occur in the colloids of senescent
              porcine pituitary glands are clusterin and glycosylated
              albumin fragments.
#cross-references MUID:97318844
#accession   JC5535
#molecule_type DNA
#residues    1-446 ##label OGA
#accession   PC4475
#molecule_type protein
#residues    58-66:68-77; 229-247; 249-251; 408-436 ##label OGT
#experimental_source pituitary gland
#note        #domain signal sequence #status predicted #label SIG\
              #domain clusterin beta chain #status predicted #label
              BCN\
              #domain clusterin alpha chain #status predicted #label
              ACH
SUMMARY        #length 446 #molecular-weight 51774 #checksum 562
              5.5% Score 96; DB 2; Length 446;
              Best Local Similarity 23.5%; Pred. No. 5.45e-01;
              Matches 8; Conservative 19; Mismatches 7; Indels 0; Gaps 0;

Db 223 SRFANIMPFLFDLNYHMFQPFDMHQAQ 256
OY 112 TOLMNIYSPVAVELSHENLYVSELETVNPH 145

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GENETICS GLN

SUMMARY #gene nolx #length 471 #molecular-weight 51205 #checksum 7158

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Best Local Similarity 29.9%; Pred. No. 7,45e-01;  
Matches 23; Conservative 21; Mismatches 30; Indels 3; Gaps 3;

Db 156 PSMPPDKAILELLOD-PELFYAIGSGGRCGKITAKDLSEFKHNPQVAFQESQA 214  
QY 83 SDPPPSKSTVEELHEIPFLRAL-TEGDTOLNMNIVSPVAELSHHENVSFLETVN 141

Db 215 QSYAQNT-IPSDSAENA 230  
QY 142 QPHNQNVSPSNVHAP 158

RESULT 12

ENTRY MMRTS #type complete  
TITLE laminin beta-2 chain precursor - rat  
ALTERNATE\_NAMES laminin chain B3; S-laminin  
ORGANISM #formal\_name Rattus norvegicus #common\_name Norway rat  
DATE 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 16-Jul-1999

ACCESSIONS S03539  
REFERENCE #authors Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.  
#journal Nature (1989) 338:229-234  
#title A laminin-like adhesive protein concentrated in the synaptic cleft of the neuromuscular junction.  
#cross-references M01D:89159410  
#accession S03539  
#residues 1-1801 #label HUN  
##cross-references EMBL:X16563; NID:957250; PIDN:CAA4561.1; PID:957251  
COMPLEX Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin chain.

FUNCTION #description interact with cells and with other basement membrane proteins to promote differentiation, development, and cell migration  
CLASSIFICATION #superfamily laminin beta-1 chain; laminin-type EGF-like homology  
KEYWORDS basement membrane; calcium binding; cell binding; coiled coil; extracellular matrix; glycoprotein; heptad repeat; heterotrimer; nidogen binding

FEATURE 1-35  
36-1801

#domain signal sequence #status predicted #label SIG  
#product laminin beta-2 chain #status predicted #label MAT  
#domain VI #label DOM6  
#domain V #label DOM5  
#domain laminin-type EGF-like homology #label LE01  
#domain laminin-type EGF-like homology #label LE02  
#domain laminin-type EGF-like homology #label LE03  
#domain laminin-type EGF-like homology #label LE04  
#domain laminin-type EGF-like homology #status atypical #label LE05  
#domain IV #label DOM4  
#domain laminin-type EGF-like homology #label LE06  
#domain III #label DOM3  
#domain laminin-type EGF-like homology #label LE07  
#domain laminin-type EGF-like homology #label LE08  
#domain laminin-type EGF-like homology #label LE09  
#domain laminin-type EGF-like homology #label LE10  
#domain laminin-type EGF-like homology #label LE11  
#domain laminin-type EGF-like homology #label LE12  
#domain laminin-type EGF-like homology #label LE13  
#domain II, heptad repeats #label DOM2  
#domain alpha #label ALP  
#domain I, heptad repeats #label DOM1  
#disulfide\_bonds #status predicted

1311,1351,1502 #binding site carbohydrate (Asn) (covalent) #status predicted  
1193,1196,1800 #disulfide\_bonds interchain #status predicted  
SUMMARY #length 1801 #molecular-weight 196472 #checksum 8852

Query Match 5.5%; Score 96; DB 1; Length 1801;  
Best Local Similarity 36.7%; Pred. No. 5,45e-01;  
Matches 11; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Db 1041 CTCNLLGTPQRCSTDLCDPSTGQPC 1070  
QY 26 CNKALCASDVSKCLIQELCCRCRPGNCSC 55

RESULT 13

ENTRY MMMSA #type complete  
TITLE laminin alpha-1 chain precursor - mouse  
ALTERNATE\_NAMES laminin chain A1  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 16-Jul-1999

ACCESSIONS A31771; A30449; S00624; A30450; S08895; S02678; S01790;  
A30451; S14670  
REFERENCE #authors Sasaki, M.; Kleinman, H.K.; Huber, H.; Deutzmann, R.; Yamada, Y.  
#journal J. Biol. Chem. (1988) 263:16536-16544  
#title Laminin, a multidomain protein. The A chain has a unique globular domain and homology with the basement membrane proteoglycan and the laminin B chains.  
#cross-references M01D:89034134  
#accession A31771  
##molecule\_type mRNA  
##residues 1-3084 #label SAS  
##cross-references EMBL:J04064; NID:9309419; PIDN:AAA39410.1; PID:9309420

#accession A30449  
##molecule\_type protein  
##residues 183-195;570-571,'A','573-586;596-612,'X','614-617','EMK';  
630-646;1217-1222,'YPR';1226-1227;1303-1310;1498-1507;  
2033-2040,'X',2042-2043;2137-2151;2156-2178;2227-2240;  
2406-2420;2440-2451;2481-2486;2624-2639;2818-2843;  
3009-3033,'V',3035 #label SA2

REFERENCE S00624  
#authors Hartl, L.; Oberpaumer, J.; Deutzmann, R.  
#journal Eur. J. Biochem. (1988) 173:629-635  
#title The N terminus of laminin A chain is homologous to the B chains.  
#cross-references M01D:88225080  
#accession S00624  
##molecule\_type mRNA  
##residues 1-208,'T',210-334 #label HAR  
##cross-references EMBL:X07737; NID:952857; PIDN:CAA50561.1; PID:952858  
#accession A30450  
##molecule\_type protein  
##residues 311-335,'N',337-339;630-642,'D',644;692-734;737-748,'X',  
750-760,'G',762-763;765-769,'X',771,'R',773-778;  
780-786,'X',788-802,'Q',839-852,'Q',854-855,'OXO',  
859-869,'Q',871-874;1148-1158;1353-1389;1449-1459  
#label HA2  
the sequence from Fig. 7 is inconsistent with that from  
Fig. 5 in having 209-Ile, 239-Thr, and 240-Arg; the  
sequence from Fig. 7 is inconsistent with that from  
Table 1 in having 335-Thr

REFERENCE S08895  
#authors Mann, K.; Deutzmann, R.; Timpl, R.  
#journal Eur. J. Biochem. (1988) 178:71-80  
#title Characterization of proteolytic fragments of the laminin-nidogen complex and their activity in ligand-binding assays.  
#cross-references M01D:89078415  
#accession S08895  
##molecule\_type protein

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REFERENCE      #residues      153-169 #label MAN
#authors      Fujimura, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.;
#journal      Blochem. J. (1988) 252:453-461
#title        Structure and distribution of N-linked oligosaccharide chains
              on various domains of mouse tumour laminin.
#cross-references MWID:88326259
#accession    S02678
#molecule_type protein
#residues     630-642, 'D', 644:2690-2704 #label FUJ
#authors      Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbauer, I.;
#journal      Eur. J. Biochem. (1988) 177:35-45
#title        Structural study of long arm fragments of laminin. Evidence
              for repetitive C-terminal sequences in the A-chain, not
              present in the B-chains.
#cross-references MWID:89030693
#accession    S01790
#molecule_type mRNA
#residues     2538-3084 #label DEU
#cross-references EMBL:X13459; NID:955499; PIDN:CMA31807.1; PID:9818014
#accession    A30451
#molecule_type Protein
#residues     1911-1929:1997-2006:2033-2045, 'X', 2047-2054, 'X',
              2056-2066, 'X', 2068-2105:2120-2170:2182-2192, 'TR';
              2209-2216:2227-2240:2247-2251, 'X', 2253-2266:2289-2298;
              2406-2420:2424-2435:2440-2451:2461-2470:2487-2498;
              2502-2525:2538-2557:2561-2591, 'X', 2593-2594:2600-2610;
              2616-2645:2648-2655:2690-2722:2754-2780:2795-2805;
              2811-2816:2818-2834:2836-2843:2854-2858-2875, 'D', 2877-2913;
              2935-2964:2969-2976:2980-2993:2998-3005, 'A', 3007-3033,
              'V', 3035:3068-3083 #label DEZ
              2256-Val was also found
#note         A34961
#authors      Olsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola,
              S.; Sanborn, D.; Sasaki, T.; Kuyvanicml, H.; Chu, M.L.;
              Deutzmann, R.; Timpl, R.; Vitto, J.
#journal      Lab. Invest. (1989) 60:772-782
#title        Human laminin: Cloning and sequence analysis of cDNAs
              encoding A, B1 and B2 chains, and expression of the
              corresponding genes in human skin and cultured cells.
#cross-references MWID:89280632
#accession    S14670
#molecule_type protein
#residues     2424-2436:2440-2451:2461-2467:2487-2525:2550-2557;
              2561-2593:2600-2610:2616-2645:2648-2655:2690-2704;
              2707-2722:2754, 'L', 2756-2780:2795-2805:2811-2816;
              2818-2844:2858-2904, 'D', 2906-2913:2935-2942, 'T',
              2944-2964:2969-2976:2980-2993:2998-3000, 'I', 3002-3018,
              'V', 3020-3034:3068-3083 #label OLS
#complex      Laminins are trimers of an alpha-type, a beta-type, and a
              gamma-type laminin chain.
#function     interact with cells and with other basement membrane proteins
              to promote differentiation, development, and cell migration
#classification #superfamily laminin alpha-1 chain; laminin G repeat
              homology; laminin-type EGF-like homology
#keywords      basement membrane; calcium binding; cell binding; coiled
              coil; extracellular matrix; glycoprotein; heparin binding;
              heptad repeat; heterotrimer; pyroglutamic acid
#feature      1-24 #domain signal sequence #status predicted #label SIG\
              25-3084 #product laminin alpha-1 chain #status predicted #label
              MAR\
              25-277 #domain VI #label DOM6\
              277-331 #domain laminin-type EGF-like homology #label LE01\
              334-401 #domain V #label DOM5\
              404-458 #domain laminin-type EGF-like homology #label LE02\
              461-507 #domain laminin-type EGF-like homology #label LE03\
              510-519 #domain laminin-type EGF-like homology #label LE04\
              #domain laminin-type EGF-like homology #status atypical

```

```

520-715 #label LE05\
716-1166 #domain IVB #label DO4B\
716-746 #domain IIB #label DO3B\
#domain laminin-type EGF-like homology #status atypical
#label LE06\
749-795 #domain laminin-type EGF-like homology #label LE07\
798-853 #domain laminin-type EGF-like homology #label LE08\
830-834 #domain laminin-type EGF-like homology #label LE09\
856-906 #region cell attachment #status predicted\
909-955 #domain laminin-type EGF-like homology #label LE10\
958-1002 #domain laminin-type EGF-like homology #label LE11\
1005-1048 #domain laminin-type EGF-like homology #label LE12\
1051-1094 #domain laminin-type EGF-like homology #label LE13\
1097-1116 #domain laminin-type EGF-like homology #status atypical
#label LE14\
1118-1154 #domain laminin-type EGF-like homology #status atypical
#label LE15\
1147-1149 #region cell attachment (R-G-D) motif\
1157-1166 #domain laminin-type EGF-like homology #status atypical
#label LE16\
1167-1368 #domain IIV #label DO4A\
1369-1561 #domain IIV #label DO3A\
1369-1407 #domain laminin-type EGF-like homology #status atypical
#label LE17\
1410-1456 #domain laminin-type EGF-like homology #label LE18\
1459-1513 #domain laminin-type EGF-like homology #label LE19\
1516-1560 #domain laminin-type EGF-like homology #label LE20\
1562-2133 #domain I/II, heptad repeats #label DOM2\
2134-3084 #domain G #label DOM3\
2150-2308 #domain laminin G repeat homology #label LG1\
2337-2422 #domain laminin G repeat homology #label LG2\
2518-2683 #domain laminin G repeat homology #label LG3\
2748-2857 #domain laminin G repeat homology #label LG4\
2935-3082 #domain laminin G repeat homology #label LG5\
#modified site pyroglutamate carboxylic acid (Gln) (in
mature form) #status predicted\
45-79:370-374, 531,
562, 672, 808, 914,
959, 969, 1052, 1344,
1414, 1586, 1603,
1659, 1686, 1706,
1718, 1725, 1763,
1812, 1902, 1906,
1936, 1982, 1993,
2027, 2046, 2106,
2251, 2252, 2356,
2526, 2738, 2924
304-312 #binding site carbohydrate (Asn) (covalent) #status
770, 857, 1999, 2055, #disulfide bonds #status experimental\
2067, 2835 #binding site carbohydrate (Asn) (covalent) #status
845, 2102 #binding site carbohydrate (Asn) (covalent) #status
absent\
SUMMARY #length 3084 #molecular weight 338169 #checksum 7032
Query Match 5.5%; Score 96; DB 1; Length 3084;
Best Local Similarity 37.5%; Pred. No. 5, 45e-01;
Matches 15; Conservative 6; Mismatches 17; Indels 2; Gaps 2;
DB 1091 PPDVPCGCDIRGTPDTCDEGLCSGSDSGTSC-KE 1129
OY 20 LPESLSCNKALCASHVSKC-LIDELCCRCRGSCCKE 58
RESULT 14
ENTRY 151538 #type complete
TITLE metallothionein - African clawed frog
ORGANISM formal_name Xenopus laevis #common_name African clawed frog
DATE 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
ACCESSIONS 151538
REFERENCE 151538

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#authors      Saint-Jacques, E.; Seguin, C.
#journal      DNA Cell Biol. (1993) 12:329-340
#title        Cloning and nucleotide sequence of a complementary DNA
               encoding Xenopus laevis metallothionein: mRNA accumulation
               in response to heavy metals.
#cross-references MIMD:93263990
#accession     151538
#status        Preliminary: translated from GB/EMBL/DBJ
#molecule-type mRNA
##residues     1-62 ##label SAI
##cross-references GB:M6729; NID:g214585; PIDN:AA59949.1; PID:g214586
CLASSIFICATION #superfamily metallothionein
SUMMARY        #length 62 #molecular-weight 6403 #checksum 3001

Query Match      5.4%; Score 94; DB 2; Length 62;
Best Local Similarity 44.4%; Pred. No. 1,0e+00;
Matches 12; Conservative 6; Mismatches 7; Indels 2; Gaps 2;

Db 38 CPACSKC-SQG-CHEKSGSKKSCCN 62
On 31 CASDVSKCLDLCQCRPGEGNGSCCK 57
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13-Aug-1999

RESULT 15
ENTRY S14458 #type complete
TITLE laminin alpha-1 chain precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
13-Aug-1999
ACCESSIONS S14458; S14663; A34961
REFERENCE S14458
#authors Haaparanta, T.; Uitto, J.; Ruoslahti, E.; Engvall, E.
#journal Matrix (1991) 11:151-160
#title Molecular cloning of the cDNA encoding human laminin A chain
#cross-references MIMD:91333420
#accession S14458
#status not compared with conceptual translation
#molecule-type mRNA
##residues 1-3075 ##label HAA
REFERENCE S14663
#authors Nissinen, M.; Vuolteenaho, R.; Boot-Handford, R.; Kallunki,
P.; Tryggvason, K.
#journal Biochem. J. (1991) 276:369-379
#title Primary structure of the human laminin A chain. Limited
expression in human tissues.
#cross-references MIMD:91264789
#accession S14663
#molecule-type mRNA
##residues 1-227,'FE','230-251','MDP','255-418','E','420-518','L',
520-1022,'V','1024-1074','V','1076-1339','W','1341-1512,
'P','1514-2078','KV','2081-2628 ##label NIS
#cross-references EMBL:X58531; NID:934225; PIDN:CAA41418.1; PID:934226
REFERENCE A34961
#cross-references EMBL:X58531; NID:934225; PIDN:CAA41418.1; PID:934226
#authors Olesen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola,
S.; Sanborn, D.; Sasaki, T.; Kuivaniemi, H.; Chu, M.L.;
Deutermann, R.; Timpl, R.; Uitto, J.
#journal Lab. Invest. (1989) 60:772-782
#title Human laminin: cloning and sequence analysis of cDNAs
encoding A, B1 and B2 chains, and expression of the
corresponding genes in human skin and cultured cells.
#cross-references MIMD:89280632
#accession A34961
#status not compared with conceptual translation
#molecule-type mRNA
##residues 'W','2397-2745','L','2747-3053','L','3055-3072','PSP' ##label
OLS
#note The authors translated the codon AGA for residue 2692 as
Pro
GENETICS
#gene GDB:LA0A1: LAMA
##cross-references GDB:120135; OMIM:150320
#map position 18p11.32-18p11.22
CLASSIFICATION #superfamily laminin alpha-1 chain; laminin G repeat

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KEYWORDS      morphology; laminin-type EGF-like homology  

               basement membrane; calcium binding; cell binding; coiled  

               coil; disulfide bond; extracellular matrix; glycoprotein;  

               heparin binding; heptad repeat; heterotrimer
FEATURE
1-17          #domain signal sequence #status predicted #label SIG\
18-30705     #product laminin alpha-1 chain #status predicted #label  

              MARY\
    18-269    #domain VI #label DOM6\  

    270-516   #domain V #label DOM5\  

    370-524   #domain laminin-type EGF-like homology #label LE1\  

    377-594   #domain laminin-type EGF-like homology #label LE2\  

    377-594   #domain laminin-type EGF-like homology #label LE3\  

    377-594   #domain laminin-type EGF-like homology #label LE4\  

    454-500   #domain laminin-type EGF-like homology #status atypical\  

    503-512   #domain laminin-type EGF-like homology #status atypical\  

    517-708   #label LE5\  

    709-1159  #domain IIVB #label DO4B\  

    709-739   #domain IIRB #label DO3B\  

    709-739   #domain laminin-type EGF-like homology #status atypical\  

    709-739   #label LE6\  

    742-788   #domain laminin-type EGF-like homology #label LE7\  

    751-846   #domain laminin-type EGF-like homology #label LE8\  

    849-899   #domain laminin-type EGF-like homology #label LE9\  

    902-948   #domain laminin-type EGF-like homology #label LE10\  

    951-995   #domain laminin-type EGF-like homology #label LE11\  

    998-1041  #domain laminin-type EGF-like homology #label LE12\  

    1044-1067 #domain laminin-type EGF-like homology #label LE13\  

    1090-1109 #domain laminin-type EGF-like homology #status atypical\  

    1111-1147 #label LE14\  

    1111-1147 #domain laminin-type EGF-like homology #status atypical\  

    1150-1159 #label LE15\  

    1150-1159 #domain laminin-type EGF-like homology #status atypical\  

    1160-1361 #label LE16\  

    1362-1553 #domain IIVA #label DO4A\  

    1362-1400 #domain IIRA #label DO3A\  

    1362-1400 #domain laminin-type EGF-like homology #status atypical\  

    1403-1449 #label LE17\  

    1452-1506 #domain laminin-type EGF-like homology #label LE18\  

    1509-1553 #domain laminin-type EGF-like homology #label LE19\  

    1554-2125 #domain laminin-type EGF-like homology #label LE20\  

    2116-2120 #domain I/II, heptad repeats #label DM2\  

    2126-3075 #region cell attachment #status predicted\  

    2142-2300 #domain G #label DOMG\  

    2329-2484 #domain laminin G repeat homology #label LG1\  

    2510-2676 #domain laminin G repeat homology #label LG2\  

    2534-2536 #domain laminin G repeat homology #label LG3\  

    2739-2888 #region cell attachment (R-G-D) motif\  

    2916-3073 #domain laminin G repeat homology #label LG4\  

    38,164,555,665,763,801,838,926,952,1045,1407,1579,  

    1596,1678,1689,1698,1717,1804,1894,1898,1957,  

    1974,1991,2038,2047,2094,2098,2243,2244,2384,  

    2408,2518,2619,2729,2852,2915,  

    2983        #binding_site carbohydrate (Asn) (covalent) #status  

                predicted\  

    297-305    #disulfide_bonds #status predicted  

SUMMARY      #length 3075 #molecular_weight 337155 #checksum 7424
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Query Match 5.4%; Score 94; DB 2; Length 3075;  

Best Local Similarity 35.0%; Pred. NO. 1.0le+00;  

Matches 14; Conservative 8; Mismatches 16; Indels 2; Gaps 2;

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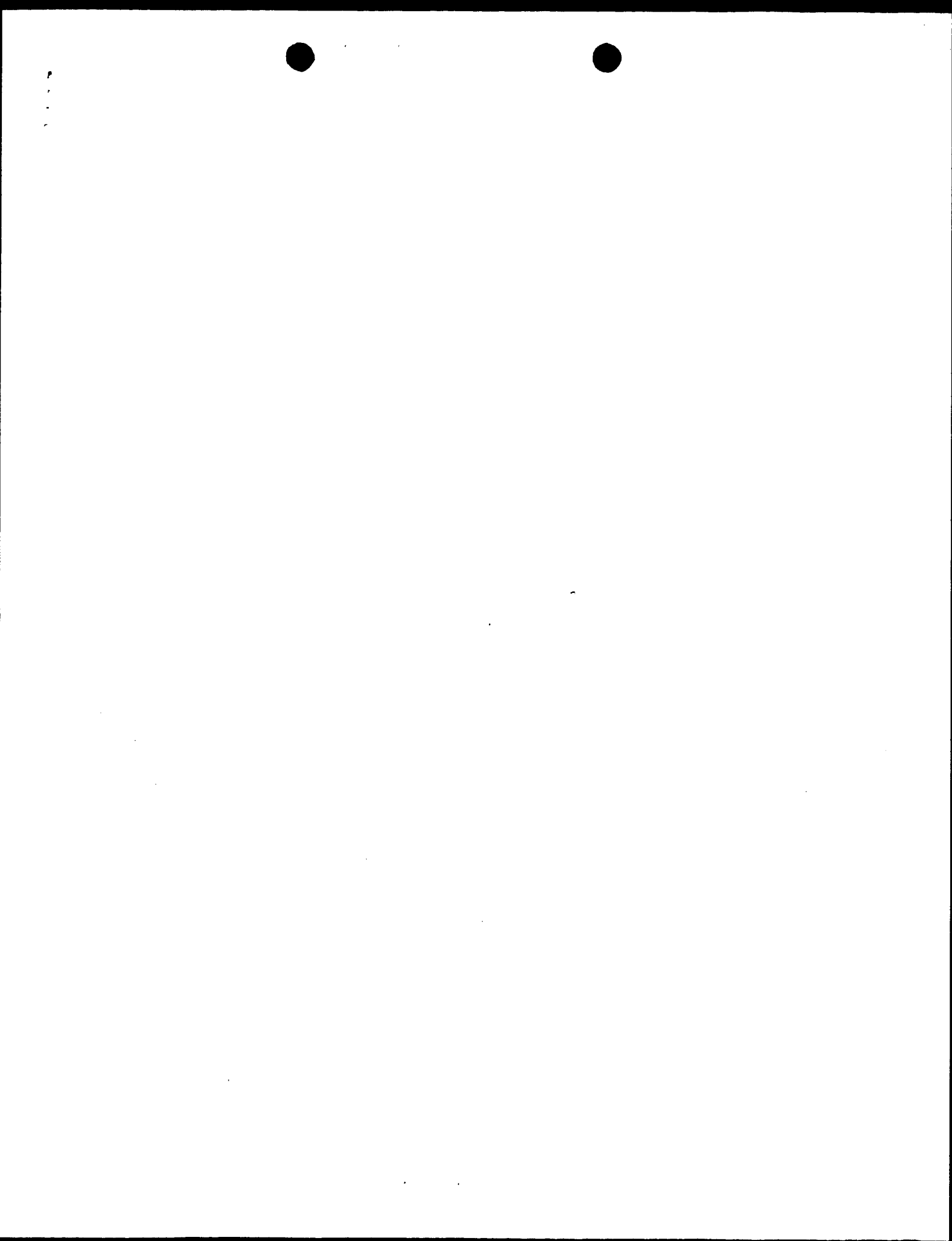
Tue Aug 29 09:10:18 2000

US-09-416-267-2.rpr

Page 9

Search completed: Wed Aug 16 09:31:22 2000  
Job time : 79 secs.

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Page 2

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AC	XXXXXX	
DT		
ID		
XX		



DE Sequence 2, Application PC/TUS9603935  
XX  
CC Sequence 2, Application PC/TUS9603935  
CC GENERAL INFORMATION:  
CC APPLICANT: LI, YI  
CC APPLICANT: SU, KUI  
CC TITLE OF INVENTION: HUMAN CYTOKINE POLYPEPTIDE  
CC NUMBER OF SEQUENCES: 9  
CC CORRESPONDENCE ADDRESSES:  
CC ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
CC ADDRESSEE: STEWART & OLSTEIN  
CC STREET: 6 BECKER FARM ROAD  
CC CITY: ROSELAND  
CC STATE: NEW JERSEY  
CC COUNTRY: USA  
CC ZIP: 07068-1739  
CC COMPUTER READABLE FORM:  
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CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US96/03935  
CC FILING DATE:  
CC CLASSIFICATION:  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Ferraro, Gregory D  
CC REGISTRATION NUMBER: 36,134  
CC REFERENCE/DOCKET NUMBER: 325800-566  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 201-994-1700  
CC TELEFAX: 201-994-1744  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 223 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 223 AA; 25017 MW; 262453 CN;  
SQ  
Query Match 100.0%; Score 1738; DB 1; Length 223;  
Best Local Similarity 100.0%; Pred. No. 6,64e-185;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MKLHYAVVLTLLIMFTLWLPESLSCNKALCASDVSKLIQELCQCRPGEGNSCKCKECM 60  
1 MLHYAVVLTLLIMFTLWLPESLSCNKALCASDVSKLIQELCQCRPGEGNSCKCKECM 60  
DB 61 LCLGALWDECCDVGKNCNPNRNSDTPPTSSTVEELHEPIPSLFRALTEGDTOLNMNIVS 120  
QY 61 LCLGALWDECCDVGKNCNPNRNSDTPPTSSTVEELHEPIPSLFRALTEGDTOLNMNIVS 120  
DB 121 FPVAEELSHENLVSELETYNOPHONVSPSNVHAPYSSDKEHMCCTVYVFDCKMSIHQ 180  
QY 121 FPVAEELSHENLVSELETYNOPHONVSPSNVHAPYSSDKEHMCCTVYVFDCKMSIHQ 180  
DB 181 CKICESMGASKYRWFHNAACECIGPECIDYGSKTIVKCNKMF 223  
QY 181 CKICESMGASKYRWFHNAACECIGPECIDYGSKTIVKCNKMF 223  
RESULT 5  
ID US-08-843-651-2 STANDARD; PRT; 223 AA.  
AC xxxxxx  
XX  
DT  
XX  
XX Sequence 2, Application US/08843651  
XX  
CC Sequence 2, Application US/08843651  
CC GENERAL INFORMATION:  
CC APPLICANT: Holtzman, Douglas

CC TITLE OF INVENTION: NOVEL PEPTIDES WITHIN THE  
CC TITLE OF INVENTION: GROWTH FACTOR SUPERFAMILY  
CC NUMBER OF SEQUENCES: 2  
CC CORRESPONDENCE ADDRESSES:  
CC ADDRESSEE: Fish & Richardson P.C.  
CC STREET: 225 Franklin Street  
CC CITY: Boston  
CC STATE: MA  
CC COUNTRY: US  
CC ZIP: 02110-2804  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Diskette  
CC COMPUTER: IBM Compatible  
CC OPERATING SYSTEM: Windows95  
CC SOFTWARE: FASTSEQ for Windows Version 2.0  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/843,651  
CC FILING DATE: 16-APR-1997  
CC PRIORITY APPLICATION DATA:  
CC APPLICATION NUMBER:  
CC FILING DATE:  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Melkielejohn, Ph.D., Anita L.  
CC REGISTRATION NUMBER: 35,283  
CC REFERENCE/DOCKET NUMBER: 09404/027001  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 617/542-5070  
CC TELEFAX: 617/542-8906  
CC TELEX: 200154  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 223 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC FRAGMENT TYPE: internal  
CC SEQUENCE 223 AA; 25017 MW; 262453 CN;  
SQ  
Query Match 100.0%; Score 1738; DB 14; Length 223;  
Best Local Similarity 100.0%; Pred. No. 6,64e-185;  
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MKLHYAVVLTLLIMFTLWLPESLSCNKALCASDVSKLIQELCQCRPGEGNSCKCKECM 60  
1 MLHYAVVLTLLIMFTLWLPESLSCNKALCASDVSKLIQELCQCRPGEGNSCKCKECM 60  
DB 61 LCLGALWDECCDVGKNCNPNRNSDTPPTSSTVEELHEPIPSLFRALTEGDTOLNMNIVS 120  
QY 61 LCLGALWDECCDVGKNCNPNRNSDTPPTSSTVEELHEPIPSLFRALTEGDTOLNMNIVS 120  
DB 121 FPVAEELSHENLVSELETYNOPHONVSPSNVHAPYSSDKEHMCCTVYVFDCKMSIHQ 180  
QY 121 FPVAEELSHENLVSELETYNOPHONVSPSNVHAPYSSDKEHMCCTVYVFDCKMSIHQ 180  
DB 181 CKICESMGASKYRWFHNAACECIGPECIDYGSKTIVKCNKMF 223  
QY 181 CKICESMGASKYRWFHNAACECIGPECIDYGSKTIVKCNKMF 223  
RESULT 6  
ID US-09-015-412-7 STANDARD; PRT; 223 AA.  
AC xxxxxx  
XX  
DT  
XX  
XX Sequence 7, Application US/09015412  
XX  
CC Sequence 7, Application US/09015412  
CC GENERAL INFORMATION:  
CC APPLICANT: Hillman, Jennifer L.  
CC APPLICANT: Lal, Preeti  
CC APPLICANT: Corley, Neil C.

Page 4

CC	Sequence 437, Application US/09330781
CC	GENERAL INFORMATION:
CC	APPLICANT: Gearing, David P.
CC	APPLICANT: Robison, Keith E.
CC	APPLICANT: Holtzman, Douglas A.
CC	TITLE OF INVENTION: Nucleic Acid Molecules Derived from a
CC	TITLE OF INVENTION: Human Prostate Stromal Cell Library
CC	FILE REFERENCE: MLN98-26PA
CC	CURRENT APPLICATION NUMBER: US/09/330,781
CC	CURRENT FILING DATE: 1999-06-11
CC	EARLIER APPLICATION NUMBER: 60/090,179
CC	EARLIER FILING DATE: 1998-06-22
CC	NUMBER OF SEQ ID NOS: 490
CC	SOFTWARE: fastseq for Windows Version 3.0
CC	SEQ ID NO 437
CC	LENGTH: 113
CC	TYPE: PRF
CC	ORGANISM: Homo sapiens
CC	FEATURE:
CC	NAME/KEY: SIGNAL
CC	LOCATION: (1)...(25)
CC	NAME/KEY: VARIANT
CC	LOCATION: (1)...(113)
CC	OTHER INFORMATION: xaa - Any Amino Acid
90	SEQUENCE 113 AA: 12537 MW: 64090 CN:

Accession	Sequence	Length
D0	1 MKLHYAVLTLALIMFLVLPESLSCNRLCASDYSKCLIDELQCRPGSGNSCKREK	60
QY	1 MKLHYAVLTLALIMFLVLPESLSCNRLCASDYSKCLIDELQCRPGSGNSCKREK	60
D0	61 LCLGALMDECCDVGNCNRRNSDTPYTSKSTVEELADPLDLSFRAL	107
QY	61 LCLGALMDECCDVGNCNRRNSDTPYTSKSTVEELADPLDLSFRAL	107

RESULT	ID	US-60-169-629-463	STANDARD;	PRT;	125 AA.
XX	AC	xxxxxx			
XX	DT				
XX	DE	Sequence 463, Application US/60169629			
CC	CC	Sequence 463, Application US/60169629			
CC	CC	GENERAL INFORMATION:			
CC	CC	APPLICANT: Dumas Milne Edwards, J. B.			
CC	CC	APPLICANT: Bougueleret, L.			
CC	CC	APPLICANT: Jobert, S.			
CC	CC	TITLE OF INVENTION: GDMS for Secreted Proteins			
CC	CC	FILE REFERENCE: GENSET 071PRF			
CC	CC	CURRENT APPLICATION NUMBER: US/60/169,629			
CC	CC	CURRENT FILING DATE: 1999-12-08			
CC	CC	NUMBER OF SEQ ID NOS: 715			
CC	CC	SOFTWARE: Patent.pm			
CC	CC	SEQ ID NO 463			
CC	CC	LENGTH: 125			
CC	CC	TYPE: PRT			
CC	CC	ORGANISM: Homo sapiens			
CC	CC	FEATURE:			
CC	CC	NAME/KEY: SIGNAL			
CC	CC	LOCATION: -14...-1			
CC	CC	SEQUENCE - 125 AA; 13870 MW; 87972 CN;			
50					

Query Match	43.8%	Score 761	DB 3	Length 125
Best Local Similarity	93.8%	Pred. No. 5,91e-71		
Matches 106	Conservative 2	Mismatches 4	Indels 1	Gaps 1

QY 60 MLCIGALWDECCDCVGMCPNRYSDTPTSKSTVEELHEPIPSLFRALTEGDTOLNMNIV 119  
DB 61 SFPVAEELSHHENLVSFLETVNOPHONVSPSNNVHAPYSSDKGN-CQQLTF 112  
QY 120 SFPVAEELSHHENLVSFLETVNOPHONVSPSNNVHAPYSSDKHEMCTVYVF 172

RESULT 9  
ID US-60-187-470-463 STANDARD: PRT: 125 AA.

DE Sequence 463, Application US/60187470

CC GENERAL INFORMATION:  
CC APPLICANT: Dumas Milne Edwards, J.B.

CC APPLICANT: Bougueleret, L.

CC TITLE OF INVENTION: CDNAS for Secreted Proteins

CC FILE REFERENCE: 78.US2.PRO

CC CURRENT APPLICATION NUMBER: US/60/187,470

CC NUMBER OF SEQ ID NOS: 715

CC SOFTWARE: Patent.pm

CC SEQ ID NO 463

CC LENGTH: 125

CC TYPE: PRT

CC ORGANISM: Homo sapiens

CC FEATURE:  
CC NAME/KEY: SIGNAL

CC LOCATION: -14...-1

CC SEQUENCE 125 AA; 13870 MW; 87972 CN;

Query Match 43.8%; Score 761; DB 3; Length 125;  
Best Local Similarity 93.8%; Pred. No. 5,91e-71;  
Matches 106; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

DB 1 MLCIGALWDECCDCVGMCPNRYSDTPTSKSTVEELHEPIPSLFRALTEGDTOLNMNIV 60  
QY 60 MLCIGALWDECCDCVGMCPNRYSDTPTSKSTVEELHEPIPSLFRALTEGDTOLNMNIV 119  
QY 61 SFPVAEELSHHENLVSFLETVNOPHONVSPSNNVHAPYSSDKGN-CQQLTF 112  
QY 120 SFPVAEELSHHENLVSFLETVNOPHONVSPSNNVHAPYSSDKHEMCTVYVF 172

RESULT 10  
ID US-60-197-873-14313 STANDARD: PRT: 128 AA.

AC xxxxxx

DE Sequence 14313, Application US/60197873

CC GENERAL INFORMATION:  
CC APPLICANT: Bejain, Stephanie

CC APPLICANT: Tanaka, Hiroaki

CC APPLICANT: Dumas Milne Edwards, Jean Baptiste

CC APPLICANT: Jobert, Severin

CC APPLICANT: Giordano, Jean-Yves

CC TITLE OF INVENTION: ESTs and Encoded Human Proteins.

CC FILE REFERENCE: 81.US1.PRO

CC CURRENT APPLICATION NUMBER: US/60/197,873

CC NUMBER OF SEQ ID NOS: 52153

CC SOFTWARE: Patent.pm

CC SEQ ID NO 14313

CC LENGTH: 128  
CC TYPE: PRT  
CC ORGANISM: Homo sapiens  
CC FEATURE:  
CC NAME/KEY: SIGNAL  
CC LOCATION: -14...-1  
QY SEQUENCE 128 AA; 14367 MW; 96202 CN;

Query Match 43.8%; Score 761; DB 23; Length 128;  
Best Local Similarity 93.8%; Pred. No. 5,91e-71;  
Matches 106; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

DB 1 MLCIGALWDECCDCVGMCPNRYSDTPTSKSTVEELHEPIPSLFRALTEGDTOLNMNIV 60  
QY 60 MLCIGALWDECCDCVGMCPNRYSDTPTSKSTVEELHEPIPSLFRALTEGDTOLNMNIV 119  
DB 61 SFPVAEELSHHENLVSFLETVNOPHONVSPSNNVHAPYSSDKGN-CQQLTF 112  
QY 120 SFPVAEELSHHENLVSFLETVNOPHONVSPSNNVHAPYSSDKHEMCTVYVF 172

RESULT 11  
ID US-60-147-499-4240 STANDARD: PRT: 128 AA.

AC xxxxxx

DE Sequence 4240, Application US/60147499

CC GENERAL INFORMATION:  
CC APPLICANT: Dumas Milne Edwards, J.B.

CC APPLICANT: Jobert, S.

CC APPLICANT: Giordano, J.Y.

CC TITLE OF INVENTION: ESTs and Encoded Human Proteins.

CC FILE REFERENCE: GENSET.054PR2

CC CURRENT APPLICATION NUMBER: US/60/147,499

CC NUMBER OF SEQ ID NOS: 19335

CC SOFTWARE: Patent.pm

CC SEQ ID NO 4240

CC LENGTH: 128

CC TYPE: PRT

CC ORGANISM: Homo sapiens

CC FEATURE:  
CC NAME/KEY: SIGNAL

CC LOCATION: -14...-1

CC SEQUENCE 128 AA; 14367 MW; 96202 CN;

Query Match 43.8%; Score 761; DB 3; Length 128;  
Best Local Similarity 93.8%; Pred. No. 5,91e-71;  
Matches 106; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

DB 1 MLCIGALWDECCDCVGMCPNRYSDTPTSKSTVEELHEPIPSLFRALTEGDTOLNMNIV 60  
QY 60 MLCIGALWDECCDCVGMCPNRYSDTPTSKSTVEELHEPIPSLFRALTEGDTOLNMNIV 119  
DB 61 SFPVAEELSHHENLVSFLETVNOPHONVSPSNNVHAPYSSDKGN-CQQLTF 112  
QY 120 SFPVAEELSHHENLVSFLETVNOPHONVSPSNNVHAPYSSDKHEMCTVYVF 172

RESULT 12  
ID US-09-307-140-1146 STANDARD: PRT: 75 AA.

AC xxxxxx

DE Sequence 1146, Application US/09307140

CC GENERAL INFORMATION:  
CC APPLICANT: Dumas Milne Edwards, Jean Baptiste

CC APPLICANT: Jobert, Severin

CC APPLICANT: Giordano, Jean-Yves

CC TITLE OF INVENTION: ESTs and Encoded Human Proteins.

CC FILE REFERENCE: 81.US1.PRO

CC CURRENT APPLICATION NUMBER: US/09/307,140

CC NUMBER OF SEQ ID NOS: 52153

CC SOFTWARE: Patent.pm

CC SEQ ID NO 1146

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CC CC TELEFAX: 301-309-8512
CC CC INFORMATION FOR SEQ ID NO: 9:
CC CC SEQUENCE CHARACTERISTICS:
CC CC LENGTH: 206 amino acids
CC CC TYPE: amino acid
CC CC STRANDEDNESS: single
CC CC TOPOLOGY: linear
CC CC MOLECULE TYPE: protein
CC CC SEQUENCE 206 AA; 22216 MW; 187648 CN;

Query Match 31.2%; Score 542; DB 14; Length 206;
Best Local Similarity 35.4%; Pred. No. 5,34e-46;
Matches 79; Conservative 55; Mismatches 70; Indels 19; Gaps

Db 1 MOLLCFVILFVIGIAPW--SSLANDGCGENEYVGSYSKCLITGSOCKKIND--CHCCKDC 57
Qy 1 MKLH-YVAVITAIILMELTWLPESLSCKKALCASDYSKCLIDELCOCRPGBSNCSCKEC 59
Db 58 LNCIGELIYECGGLDMC-PHKDVLPSPRSEIGDI-EGVPELFDITLAEDE-GWST 114
Qy 60 MLCIGALMPECCDCVGMKNPRYSPTDP--TSKSYVEELHPIPSLFRALTEGDLQNMNI 118
Db 115 IFSMAGTKR---VA--QG-GAS--GDGNGNGNGNAG-SAGVT-LCTIYI-NSCIRA 166
Qy 119 VSPFVAEEISHENLVSLEFVYNOPPHQONVSPSNVVAAPSSDEKHEMCTVYTFDCKSI 178
Db 164 NKCRQCESMGASYSYRWTFHDCGECCEVGENCLANGINESRCGC 206
Qy 179 HCKICSESGASKYRWRHNNCCGICIDGISTVYACMNC 221

RESULT 14
ID PCT-US96-03935-9 STANDARD; PRF; 206 AA.
XX xxxxxx
XX
XX Sequence 9, Application PC/TUS9603935
XX
XX Sequence 9, Application PC/TUS9603935
XX CC GENERAL INFORMATION:
XX CC APPLICANT: LI, YI
XX CC APPLICANT: SU, KUI
XX CC TITLE OF INVENTION: HUMAN CYTOKINE POLYPEPTIDE
XX CC NUMBER OF SEQUENCES: 9
XX CC CORRESPONDENCE ADDRESS:
XX CC ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
XX CC ADDRESS: CARMELA & OLSTEIN
XX CC STREET: 6 BECKER FARM ROAD
XX CC CITY: ROSELAND
XX CC STATE: NEW JERSEY
XX CC COUNTRY: USA
XX CC ZIP: 07068-1739
XX CC COMPUTER READABLE FORM:
XX CC MEDIUM TYPE: Floppy disk
XX CC COMPUTER: IBM PC compatible
XX CC OPERATING SYSTEM: PC-DOS/MS-DOS
XX CC SOFTWARE: Patentin Release #1.0, Version #1.30
XX CC CURRENT APPLICATION DATA:
XX CC APPLICATION NUMBER: PCT/US96/03935
XX CC FILING DATE:
XX CC CLASSIFICATION:
XX CC ATTORNEY/AGENT INFORMATION:
XX CC NAME: Ferraro, Gregory D
XX CC REGISTRATION NUMBER: 36,134
XX CC REFERENCE/DOCKET NUMBER: 328800-566
XX CC TELECOMMUNICATION INFORMATION:
XX CC TELEPHONE: 201-994-1700
XX CC TELEFAX: 201-994-1744
XX CC INFORMATION FOR SEQ ID NO: 9:
XX CC SEQUENCE CHARACTERISTICS:
XX CC LENGTH: 206 amino acids
XX CC

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CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
SQ SEQUENCE 206 AA; 22216 MM; 187648 CN;

Query Match 31.2%; Score 542; DB 1; Length 206;  
Best Local Similarity 35.4%; Pred. No. 5.34e-46;  
Matches 79; Conservative 55; Mismatches 70; Indels 19; Gaps 14;

Db 1 MOLLCFYILFVGIAPW-SSLANDGCNEVYCGSVSKCLITOSCCKLND--CHCKKDC 57  
QY 1 MKLH-YVAVLTALIMFLTWLPESLSCNKALCASDVSKCLIQELCOCRPGEGNCSCCKEC 59  
Db 58 LNCGLGEYIECCGCLDMC-PKHKDVLPSTLRSEIGDI-EGVPELFDTLTAEDDE-GWST 114  
QY 60 MLCIGALMDECCDCVGMCPNRYSDTTP-TSKSTVEELHEPIPSLFRALTEGDTQLNMNI 118  
Db 115 IFRSMRAGFRQR--VA--QG-GAS--GDAGNGNGNAG-SAGVT-LCTVIY-NSCIRA 163  
QY 119 VSEFVAEELSHENLVSPLETYNQPHQNVSVPSNNVHAPYSSDKEMCTVYFFDCMSI 178  
Db 164 NKCRQCESMGASSYRMFHDGCECEVGENCLNNGINESRCRC 206  
QY 179 HQCKISCSMGASKYRMFHNACCECIGPECIDYGSKTVCAMC 221

RESULT 15  
ID US-09-416-267-9 STANDARD; PRT: 206 AA.  
XX xxxxxx  
XX DT  
XX

Sequence 9, Application US/09416267

CC Sequence 9, Application US/09416267  
CC GENERAL INFORMATION:  
CC APPLICANT: LI, YI  
CC APPLICANT: SU, KUI  
CC APPLICANT: LI, HAODONG  
CC TITLE OF INVENTION: HUMAN CYTOKINE POLYPEPTIDE  
CC NUMBER OF SEQUENCES: 9  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Human Genome Sciences, Inc.  
CC STREET: 9410 Key West Avenue  
CC CITY: Rockville  
CC STATE: MD  
CC COUNTRY: USA  
CC ZIP: 20850  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/09/416,267  
CC FILING DATE: OCT-12-1999  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Joseph J. Kenny  
CC REGISTRATION NUMBER: 43,710  
CC REFERENCE/DOCKET NUMBER: PF270P1  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 301-309-8504  
CC TELEFAX: 301-309-8439  
CC INFORMATION FOR SEQ ID NO: 9:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 206 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein

SQ SEQUENCE 206 AA; 22216 MM; 187648 CN;  
Query Match 31.2%; Score 542; DB 20; Length 206;  
Best Local Similarity 35.4%; Pred. No. 5.34e-46;  
Matches 79; Conservative 55; Mismatches 70; Indels 19; Gaps 14;

Db 1 MOLLCFYILFVGIAPW-SSLANDGCNEVYCGSVSKCLITOSCCKLND--CHCKKDC 57  
QY 1 MKLH-YVAVLTALIMFLTWLPESLSCNKALCASDVSKCLIQELCOCRPGEGNCSCCKEC 59  
Db 58 LNCGLGEYIECCGCLDMC-PKHKDVLPSTLRSEIGDI-EGVPELFDTLTAEDDE-GWST 114  
QY 60 MLCIGALMDECCDCVGMCPNRYSDTTP-TSKSTVEELHEPIPSLFRALTEGDTQLNMNI 118  
Db 115 IFRSMRAGFRQR--VA--QG-GAS--GDAGNGNGNAG-SAGVT-LCTVIY-NSCIRA 163  
QY 119 VSEFVAEELSHENLVSPLETYNQPHQNVSVPSNNVHAPYSSDKEMCTVYFFDCMSI 178  
Db 164 NKCRQCESMGASSYRMFHDGCECEVGENCLNNGINESRCRC 206  
QY 179 HQCKISCSMGASKYRMFHNACCECIGPECIDYGSKTVCAMC 221

Search completed: Wed Aug 16 09:40:22 2000  
Job time : 277 secs.





Db 1 MKLHYAVLTALITLMTLPESLSCKNALCASDVSKCLIOELCCRRGEGNSCCCKECM 60  
 QY 1 MKLHYAVLTALITLMTLPESLSCKNALCASDVSKCLIOELCCRRGEGNSCCCKECM 60  
 Db 61 LCLGALMDECCDCVGMCPNRYSDPTPTSKSTVEELHEPIPSLFRALTEGDTQLNMNIVS 120  
 QY 61 LCLGALMDECCDCVGMCPNRYSDPTPTSKSTVEELHEPIPSLFRALTEGDTQLNMNIVS 120  
 Db 121 FPVAEELSHHENIVSELTYNQPHONVSPSNVHAPYSSDKRHKMCTVYVFDQMSIHQ 180  
 QY 121 FPVAEELSHHENIVSELTYNQPHONVSPSNVHAPYSSDKRHKMCTVYVFDQMSIHQ 180  
 Db 181 CRISCEMGAASKYRMFHNACCECIGPECIDYGSKTVKCMNCF 223  
 QY 181 CRISCEMGAASKYRMFHNACCECIGPECIDYGSKTVKCMNCF 223

RESULT 2  
 ID W0591 standard; Protein; 223 AA.  
 AC W0591;  
 DT 15-FEB-1999 (first entry)  
 Human growth factor Tango-67.  
 Tango-67; growth factor; human; inflammation; cell proliferation;  
 therapy; diagnosis; wound healing; tissue repair; vulnery.  
 OS Homo sapiens.  
 PN W09846641-A1.  
 PD 22-OCT-1998.  
 PF 15-APR-1998; U07603.  
 PR 16-APR-1997; US-843651.  
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
 PI Holzman D;  
 DR WPI; 98-609915/51.  
 N-PSDB; V63465.  
 PT New isolated growth factor, Tango-67 - used to develop products for  
 the diagnosis and treatment of inflammation or disorders associated  
 PT with cellular proliferation  
 PS Claim 5; Fig 1; 69pp; English.  
 CC This is the amino acid sequence of Tango-67, a novel human soluble  
 CC growth factor which is capable of promoting cell proliferation  
 CC and/or differentiation. The sequence was deduced from the  
 CC nucleotide sequence (see V63465) of a cDNA clone obtained from a  
 CC human astrocyte cDNA library. Tango-67 is related to a number of  
 CC growth factors, particularly members of the connective tissue  
 CC growth factor family such as TSG. The invention provides Tango-67  
 CC nucleic acid molecules and polypeptides, host cells, vectors and  
 CC antibodies. The products can be used for the treatment of  
 CC disorders associated with aberrant expression or activity of  
 CC Tango-67. In particular they can be used to diagnose or treat  
 CC inflammation or disorders associated with cellular proliferation.  
 CC The Tango-67 polypeptides can be used in wound healing, tissue  
 CC repair, implant fixation, or stimulation of bone growth. The  
 CC products can also be used for detection, diagnosis and screening  
 CC assays.  
 SQ Sequence 223 AA:

Query Match 100.0%; Score 1738; DB 1; Length 223;  
 Best Local Similarity 100.0%; Pred. No. 8,73e-158;  
 Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 CRISCEMGAASKYRMFHNACCECIGPECIDYGSKTVKCMNCF 223

RESULT 3  
 ID Y13362 standard; Protein; 420 AA.  
 AC Y13362;  
 DT 25-JUN-1999 (first entry)  
 Amino acid sequence of protein PRO214.  
 DE Secreted protein; transmembrane protein; human; enterocolitis;  
 KW Zollinger-Ellison syndrome; gastrointestinal ulceration;  
 KW congenital microvillus atrophy; skin disease; cell growth;  
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;  
 KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;  
 KW fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;  
 KW anti-thrombotic; wound healing; tissue repair.  
 OS Homo sapiens.  
 PN W09914328-A2.  
 PD 25-MAR-1999.  
 PF 16-SEP-1998.  
 PR 25-NOV-1997; U19330.  
 PR 17-SEP-1997; US-066840.  
 PR 17-SEP-1997; US-059113.  
 PR 17-SEP-1997; US-059115.  
 PR 17-SEP-1997; US-059117.  
 PR 17-SEP-1997; US-059119.  
 PR 17-SEP-1997; US-059121.  
 PR 17-SEP-1997; US-059122.  
 PR 17-SEP-1997; US-059184.  
 PR 18-SEP-1997; US-059263.  
 PR 18-SEP-1997; US-059266.  
 PR 15-OCT-1997; US-062125.  
 PR 17-OCT-1997; US-062285.  
 PR 17-OCT-1997; US-062287.  
 PR 21-OCT-1997; US-063486.  
 PR 24-OCT-1997; US-062814.  
 PR 24-OCT-1997; US-063045.  
 PR 24-OCT-1997; US-063120.  
 PR 24-OCT-1997; US-063121.  
 PR 24-OCT-1997; US-063127.  
 PR 24-OCT-1997; US-063128.  
 PR 27-OCT-1997; US-063329.  
 PR 27-OCT-1997; US-063327.  
 PR 28-OCT-1997; US-063541.  
 PR 28-OCT-1997; US-063542.  
 PR 28-OCT-1997; US-063544.  
 PR 28-OCT-1997; US-063549.  
 PR 28-OCT-1997; US-063550.  
 PR 28-OCT-1997; US-063564.  
 PR 29-OCT-1997; US-063435.  
 PR 29-OCT-1997; US-063704.  
 PR 29-OCT-1997; US-063732.  
 PR 29-OCT-1997; US-063738.  
 PR 29-OCT-1997; US-063734.  
 PR 29-OCT-1997; US-064215.  
 PR 29-OCT-1997; US-064215.  
 PR 31-OCT-1997; US-063870.  
 PR 31-OCT-1997; US-064109.  
 PR 03-NOV-1997; US-064248.  
 PR 07-NOV-1997; US-064809.  
 PR 12-NOV-1997; US-065186.  
 PR 17-NOV-1997; US-065186.  
 PR 18-NOV-1997; US-065693.  
 PR 21-NOV-1997; US-066120.  
 PR 21-NOV-1997; US-066364.  
 PR 24-NOV-1997; US-066772.  
 PR 24-NOV-1997; US-066466.  
 PR 24-NOV-1997; US-066770.  
 PR 24-NOV-1997; US-066511.  
 PR 24-NOV-1997; US-066543.  
 PA (GETH) GENENTECH INC.  
 PI Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;  
 DR WPI; 99-229533/19.  
 N-PSDB; X52233.



PT New isolated human genes and polypeptides used in, e.g. treatment of  
PT gastrointestinal ulceration  
PS Claim 12, Fig 40; 320pp; English.  
CC Y13344-403 represent secreted and transmembrane human proteins.  
CC The cDNA sequences are obtained from cDNA libraries, prepared from  
CC fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.  
CC The encoded polypeptides have specific uses based on their homology to  
CC known polypeptides, e.g. PRO211 and PRO217 can be used for disorders  
CC associated with the preservation and maintenance of gastrointestinal  
CC mucosa and the repair of acute and chronic mucosal lesions  
CC (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal  
CC ulceration and congenital microvillus atrophy), skin diseases associated  
CC with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial  
CC cancers such as lung squamous cell carcinoma of the vulva and gliomas),  
CC potent effects on cell growth and development, diseases related to growth  
CC or survival of nerve cells including Parkinson's disease, Alzheimer's  
CC disease, ALS, neuropathies or cancer. PRO265 can be used as for  
CC fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used  
CC as a target for anti-tumor drugs. PRO303 may be used in the treatment  
CC of Usher Syndrome or Atrophia areata; PRO269 can be used as an  
CC anti-thrombotic agent; PRO287 polypeptides and portions may have  
CC therapeutic applications in wound healing and tissue repair; PRO317 can  
CC be used for treating problems of the kidney, uterus, endometrium, blood  
CC vessels, or related tissue, e.g. in the heart of genital tract.  
Sequence 420 AA;

```

:Query Match      5.8%      Score 100; DB 1; Length 420;
:Best Local Similarity 28.6%      Pred. No. 8, 28+00;
:Matches          14; Conservative 12; Mismatches 21; Indels 2; Gaps 2;

Db      236 WALHIHKVLDDEGTGEGANGAGDQFCVYNTGSTGECRCARACIGCGMA 284
      19 WLPBLSLC-NKALDASDVSKCLIDELQCRPGEINC-SCCEKTCITLIGA 65

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Db 236 WALHLKCVDIDECGETEGANCADQFCVNTGSEYECRDKAKACLGCMGA 28  
 19 WLPELSLC-NKALCASDVSKCLIQLCLQCQRPGEINC-SCCKECMLCLGA 65

RESULT	4
ID	V05281 standard; Protein; 420 AA.
AC	v05281;
DT	22-JUN-1999 (first entry)
DE	Egf-like homologue PRO214.
KW	Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246;
KM	EBF-2; Inhibitor; tumour growth; cancer; EGF-like homologue;
KW	EGF-8 homologue.
OS	Homo sapiens.
SN	X09914327.f2.
TS	25-MAR-1999.
TI	10-SEP-1998; U18824.
PR	25-NOV-1997; US-066840.
PR	17-SEP-1997; US-059114.
PR	17-SEP-1997; US-059117.
PR	18-SEP-1997; US-059262.
PR	15-OCT-1997; US-062123.
PR	17-OCT-1997; US-062285.
PR	17-OCT-1997; US-062287.
PR	24-OCT-1997; US-062816.
PR	29-OCT-1997; US-063704.
PA	(GETH ) GENENTECH INC.
PI	Botstein D, Goddard A, Gurney A, Hillan K, Lawrence DA,
PI	Roy M, Wood WT.
DR	NPI; 99-229532/19.
DR	N-SDB; X28431.
PT	Antibodies against specific proteins overexpressed in tumours
PS	Example 1; Fig 10; 130pp; English.
CC	This sequence relates to the EGF-like homologue PRO214.
CC	The invention relates to antibodies (Ab) that bind to any of the
CC	polypeptides (1) designated PRO187; PRO533; PRO240; PRO211;
CC	PRO230; PRO261; PRO246 or EBF-2. The Ab, or other agents that inhibit
CC	expression and/or activity of (1) are used: (1) to inhibit growth of
CC	tumours; and (11) as diagnostic/prognostic reagents for detection or
CC	quantification of (1) in cells or tissues, by standard immunoassays, with
CC	overexpression being indicative of cancer. For therapeutic use, the Ab
CC	may be conjugated to a toxin, chemotherapeutic agent or radioisotope.
CC	Genes expressing (1), many of which are growth factor homologues, are

CC overexpressed in some cases of cancer.  
SQ Sequence 420 AA;

Query Match	5.88;	Score 100;	DB 1;	Length 420;
Best Local Similarity	28.6%;	Pred. No. 8.28e+00;		
Matches	14;	Conservative	12;	Mismatches 21;
			Indels	2;
			Gaps	2.

Db 236 WALHLKCVDIDECSTEGANGCAGDQFCVNTESGTECRDCAKACLGCMGA 28  
| | : :: : | : | | : ||  
QY 19 WLPESLSC-NKALCASDVSKCLIQELCQCRPGEGNC-SCCKECMLTIGA 65

19 WLPELSC-NKALCASDVSKLIQELCQCRPGENGNC-SCCKECMLCIGA 65

RESULT	5
ID	P94758 standard; protein; 3084 AA.

AL P94/58;

BT	27-JAN-1991 (first entry)
DE	Sequence of mouse laminin A chain
RT	Portaborn, mouse, 1988, 1989, 1990, 1991

Per l'ipotesi

	Location/Qualifiers
OS	mouse.
FH	Key
ET	port+140
	1 34

FT peptide

F1	protein	23.3084
PN	US7267564-A.	
PD	28-FEB-1989	

DE 07-NOV-1989 0637EC A

PR 07-NOV-1988; US-267564.

DT	Y	DUPLICATE
DT	Y	DUPLICATE

DR N-PSDB: N91779.

DNA encoding human

and new synthetic peptide(s) with laminin-type biological activity

**PS** **Disclos**

The sequence encoding mouse laminin A chain (N91779) is used as a probe to screen a human cDNA library. Laminin is a very potent and rapid

stimula

CC Sequence 3084 AA: nerve regeneration and promotes both central and peripheral

Query Match	5.68;	Score 97;	DB 1;	Length 3084;
Best Local Similarity	40.04;	Pred. No. 1.38e+01;		
Matches	16;	Conservative	5;	Mismatches 17; Indels 2; Gaps 2.

Db 1091 EPDCLPCPCHLTPTLPHTCDLEGLCSCSEDSGTCSK-KE 1129  
:::|::|

QY 20 LPESLSCNKALCASDVSKC-LIOELCOCRPGE GNCSCCKE 58

## RESULT 6

ID	W94641 standard; peptide; 77 AA.
AC	W94641;

DT 29-APR-1999 (first entry)

DE TNF-R extracellular Cys-rich domain TNF-R p75.  
 TNMour necrosis factor receptor; TNF-R; autoimmune diseases;  
 KM

KW inflammation; septic shock; cachexia; graft versus host disease;

KM skin allergic reaction; immune complex disease; malaria;  
KW transplantation rejection.

**Homo sapiens.**

PN W09853842-A1.  
PD 03-DEC-1998.  
DE 08-MAY-1998. \*\*\*00001

439-MAY-1996; 010810Z

PR 30-MAY-1997; US-866545.  
PA (TYPE-) UNIV PENNSYLVANIA.  
BT

F1 Gleeble M1, Murakami K, Takasaka W,  
F2 F1 Gleeble M1, Murakami K, Takasaka W,

DR WPI; 99-080/81/07.

receptors are capable of initiating the biological

activities of tumour necrosis factor, e.g., in treating inflammation or autoimmune diseases

20 The author, Elyse, English  
21 The author, Elyse, English

and present invention describes peptides and peptide analogues which correspond in primary sequence to a binding loop of a tumour necrosis

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Query Match      5.5%; Score 95; DB 1; Length 122
Best Local Similarity 42.4%; Pred. NO. 1.93e+01;
```

DR WPI; 98-101052/09.

DR N-PSDB; V19802.  
PT Truncated and soluble forms of tumour necrosis factor receptor =

PT useful for treating diseases involving factor, e.g. arthritis and  
 PT adult respiratory distress syndrome  
 PS Claim 3; Fig 8; 205pp; English.  
 CC This sequence is the human tumour necrosis factor inhibitor. The protein  
 CC was used to make the truncated soluble tumour necrosis factor receptor  
 CC (sTNFR) proteins of the invention. The truncated sTNFR proteins and  
 CC tumour necrosis factor binding proteins (TNBP) are used to treat any  
 CC TNF-mediated disease, e.g. arthritis, adult respiratory distress  
 CC syndrome, cachexia/anorexia, cancer, chronic fatigue syndrome, graft  
 CC rejection, Alzheimer's disease and other autoimmune diseases. Cells  
 CC transformed with a vector containing DNA encoding the protein may be used  
 CC for production of recombinant sTNFR, which may also be used for measuring  
 CC the amount of sTNFR in samples and to raise antibodies against sTNFR.  
 CC TNBP may also be used in preparation of therapeutic compositions for  
 CC treating the above diseases. The sTNFR proteins are well suited to large  
 CC scale production (since they lack the deamidation site in region 111-126,  
 CC so are more stable in vivo); contain fewer disulphide bonds and fewer  
 CC epitopes, making them less antigenic than full-length proteins.  
 CC Sequence 235 AA.

Query Match 5.5%; Score 95; DB 1; Length 235;  
 Best Local Similarity 42.4%; Pred. No. 1.93e+01;  
 Matches 25; Conservative 10; Mismatches 13; Indels 11; Gaps 11;

DB 67 WPECLSCG-SRCSDDVETACTREONRICTCRPG-WYCALSKOGGRLC-APLRK-C 121  
 QY 19 WLPESLSCKNALCASP-V-SK-CLI-QE-LCCPRGEGNCSCCK-E-CMLCIGALMDEC 70

RESULT 10  
 ID W59665 standard; Protein; 235 AA.  
 AC W59665;

DT 28-SEP-1998 (first entry)  
 DE Human soluble tumour necrosis factor receptor type II.  
 KM Human; tumour necrosis factor; TNF; TNF receptor type II;  
 KM inflammatory disease; leukaemia; TNF binding protein;  
 KM anti-inflammatory drug; methotrexates.

OS Homo sapiens.  
 PN WO9824463-A2.

PD 11-JUN-1998.  
 PR 08-DEC-1997; U22733.  
 PR 09-JUL-1997; US-052023.  
 PR 06-DEC-1996; US-032587.  
 PR 23-JAN-1997; US-036355.  
 PR 07-FEB-1997; US-039315.

(AMGE-) AMGEN INC.  
 Bendale AM, Edwards CK, Sennello RM;  
 DR N-PSDB; V41549.

PT Treatment of acute or chronic inflammatory disease, e.g. leukaemia -  
 PT by administering tumour necrosis factor binding protein and at least  
 PT one additional anti-inflammatory drug, e.g. methotrexate  
 PS Disclosure; Fig 2; 104pp; English.  
 CC This is the amino acid sequence of the human tumour necrosis factor  
 CC receptor type II, used in the method of the invention involving the  
 CC treatment of acute or chronic inflammatory disease such as leukaemia  
 CC by administering tumour necrosis factor binding protein and at least  
 CC one additional anti-inflammatory drug, e.g. methotrexate.  
 CC Sequence 235 AA;

Query Match 5.5%; Score 95; DB 1; Length 235;  
 Best Local Similarity 42.4%; Pred. No. 1.93e+01;  
 Matches 25; Conservative 10; Mismatches 13; Indels 11; Gaps 11;

DB 67 WPECLSCG-SRCSDDVETACTREONRICTCRPG-WYCALSKOGGRLC-APLRK-C 121  
 QY 19 WLPESLSCKNALCASP-V-SK-CLI-QE-LCCPRGEGNCSCCK-E-CMLCIGALMDEC 70

RESULT 11  
 ID W89234 standard; Protein; 235 AA.  
 AC W89234;  
 DT 04-MAR-1999 (first entry)

DE Tumour necrosis inhibitor 40 kDa protein.  
 KM Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;  
 KM OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
 KM inflammation; apoptosis.

OS Homo sapiens.  
 PN WO9849305-A1.  
 PD 05-NOV-1998.  
 PR 29-APR-1998; U08631.  
 PR 01-MAY-1997; US-850188.  
 PA (AMGE-) AMGEN INC.  
 PI Boyle WJ, Woodden S;  
 DR WPI; 99-034661/03.  
 DR N-PSDB; V81733.

PT New chimeric osteoprotegerin polypeptides - contain the  
 PT osteoprotegerin dimerisation domain and a heterologous sequence,  
 PT useful to treat TNF and TNFR-mediated disorders  
 PS Disclosure; Fig 3; 92pp; English.

CC The present invention describes a chimeric polypeptide (A1), comprising  
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
 CC amino acid sequence. Also described are: (1) a multimer polypeptide  
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic  
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid  
 CC sequence; and (4) a host cell transformed or transfected with the  
 CC expression vector so that the nucleic acid is expressible. The products  
 CC from the present invention are useful to treat a variety of disorders  
 CC including those related to receptor binding. Compositions comprising  
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
 CC autoimmune diseases and disorders related to excessive apoptosis. The  
 CC chimeras are also useful for detecting molecules which interact with  
 CC fused heterologous sequences to identify potential new receptors and  
 CC ligands. The present sequence represents the TNF inhibitor 40 kDa  
 CC protein.  
 CC Sequence 235 AA;

Query Match 5.5%; Score 95; DB 1; Length 235;  
 Best Local Similarity 42.4%; Pred. No. 1.93e+01;  
 Matches 25; Conservative 10; Mismatches 13; Indels 11; Gaps 11;

DB 67 WPECLSCG-SRCSDDVETACTREONRICTCRPG-WYCALSKOGGRLC-APLRK-C 121  
 QY 19 WLPESLSCKNALCASP-V-SK-CLI-QE-LCCPRGEGNCSCCK-E-CMLCIGALMDEC 70

RESULT 12  
 ID R72504 standard; Protein; 461 AA.

DT 31-OCT-1995 (first entry)  
 DE p75 Tumour Necrosis Factor Receptor.  
 KM Ligand; tumour necrosis factor; nerve growth factor; TNF; NGF;  
 KM receptor.  
 OS Homo sapiens.

PH Key Location/Qualifiers  
 FT region 27..214  
 FT /label= TBPII.  
 FT domain 258..285  
 FT /label= Transmembrane domain.  
 FT msc\_difference 259  
 FT /note= "Unidentified amino acid."

PN EP-648783-A.  
 PD 19-APR-1995.  
 PR 11-OCT-1994; 116015.  
 PR 12-OCT-1993; IL-107267.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 PA (WALL/) WALLACH D.  
 PI Belersky I, Bigda J, Mett I, Wallach D;  
 DR WPI; 95-148673/20.  
 DR N-PSDB; Q89544.

PT Tumour necrosis factor (TNF) receptor ligand - used to increase  
 PT inhibitory effect of a soluble TNF receptor  
 PS Disclosure; Figure 2; 18pp; English.  
 CC A ligand to a member of the tumour necrosis factor (TNF)/nerve  
 CC growth factor (NGF) receptor family which binds either to the region

CC of the 4th-Cys rich domain of the receptor, or to the region between  
 CC it and the cell membrane may be used in the production of a  
 CC pharmaceutical composition for increasing the inhibitory effect of a  
 CC soluble receptor of the TNF/NGF receptor family. This sequence  
 CC is the sequence of the p75 TNF receptor.  
 SQ Sequence 461 AA;

Query Match 5.5%; Score 95; DB 1; Length 461;  
 Best Local Similarity 42.4%; Pred. No. 1.93e+01;  
 Matches 25; Conservative 10; Mismatches 13; Indels 11; Gaps 11;

Db 89 WPECLSCG-SRCSDDVEYQACTREONRIGTCRPG-WYCALSKOEGCRIC-APLRK-C 143  
 19 WPECLSCNKLKASD-V-SK-CLI-QE-LCQCRPGSGNSCK-E-CMLCLGALWDEC 70

RESULT 13  
 ID R11001 standard; Protein; 461 AA.  
 AC R11001;  
 DT 13-MAY-1991 (first entry)  
 DE 40KD TNF inhibitor precursor.  
 DE Tumour necrosis factor; inhibitor.  
 DE Homo sapiens.  
 AU058976-A.  
 PD 24-JAN-1991.  
 PE 16-JUL-1990; 058976.  
 PR 18-JUL-1989; US-381080.  
 PR 11-DEC-1989; US-450329.  
 PR 07-FEB-1990; US-479661.  
 PA (SYNE-) SYNERGEN INC.  
 DR WPI; 91-073847/11.  
 DR N-PSDB; 010907.  
 PT Tumour necrosis factor inhibitor - for suppression of TNF-alpha  
 PT and -beta, useful as therapeutic agent.  
 PS Disclosure; Fig 39; 14pp; English.  
 CC The sequence comprises the entire 40 KD TNF inhibitor. The clone  
 CC from which the sequence was isolated from a cDNA  
 CC library prep. from RNA from U937 cells treated with PMA/PHA.  
 CC The whole gene can be inserted into expression vectors for prepn.  
 CC of TNF inhibitor for use in the treatment of inflammatory and  
 CC degenerative diseases.  
 CC See also R10986 and R10984.  
 CE Sequence 461 AA;  
 SQ

Query Match 5.5%; Score 95; DB 1; Length 461;  
 Best Local Similarity 42.4%; Pred. No. 1.93e+01;  
 Matches 25; Conservative 10; Mismatches 13; Indels 11; Gaps 11;

Db 89 WPECLSCG-SRCSDDVEYQACTREONRIGTCRPG-WYCALSKOEGCRIC-APLRK-C 143  
 19 WPECLSCNKLKASD-V-SK-CLI-QE-LCQCRPGSGNSCK-E-CMLCLGALWDEC 70

RESULT 14  
 ID R11141 standard; Protein; 461 AA.  
 AC R11141;  
 DT 24-MAY-1991 (first entry)  
 DE Human TNF-R deduced from clone 1.  
 DE Tumour necrosis factor receptor; immune response; inflammation;  
 KW cachexia; septic shock.  
 OS Homo sapiens.  
 FH Key  
 FT peptide  
 FT 1. .22  
 FT /label= signal sequence  
 FT protein  
 FT 23. .461  
 FT /label= TNF receptor  
 FT domain  
 FT 258. .287  
 FT /label= transmembrane region

EP-418014-A.  
 PD 20-MAR-1991.  
 PD 10-SEP-1990; 309875.  
 PR 11-SEP-1989; US-405370.  
 PR 13-OCT-1989; US-421417.

PR 10-MAY-1990; US-523635.  
 PA (IMV-) IMMUNEX CORP.  
 PI Smith CA, Goodwin RG, Beckmann PM;  
 DR WPI; 91-082230/12.  
 DR N-PSDB; 010990.  
 PT New tumour necrosis factor -alpha and -beta receptors - and DNA  
 PT encoding these used to regulate immune responses in treatment of  
 FT cachexia, septic shock or side-effects of cytokine therapy.  
 PS Disclosure; Fig 2; 41pp; English.  
 CC The sequence was deduced from a DNA sequence obtd. from a clone  
 CC isolated from a library prep. from a human fibroblast cell line,  
 CC WI-26 V44 (ATCC CCL 95.1). The clone is deposited as Accession No.  
 CC 68088 under the name pCAV/NOT-TNF-R. The DNA can be truncated to  
 CC produce sequences which express soluble receptor comprising  
 CC residues 1-235, 1-185 or 1-163 of the protein.  
 CC See also R11142.  
 CC Sequence 461 AA;  
 SQ

Query Match 5.5%; Score 95; DB 1; Length 461;  
 Best Local Similarity 42.4%; Pred. No. 1.93e+01;  
 Matches 25; Conservative 10; Mismatches 13; Indels 11; Gaps 11;

Db 89 WPECLSCG-SRCSDDVEYQACTREONRIGTCRPG-WYCALSKOEGCRIC-APLRK-C 143  
 19 WPECLSCNKLKASD-V-SK-CLI-QE-LCQCRPGSGNSCK-E-CMLCLGALWDEC 70

RESULT 15  
 ID R42058 standard; Protein; 461 AA.  
 AC R42058;  
 DT 29-APR-1994 (first entry)  
 DE Fibroblast derived TNF-R.  
 DE Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;  
 KW IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;  
 KW rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;  
 KW pulmonary fibrosis; siliocosis; allograft; xenograft; rejection;  
 KW graft versus host disease; sepsis; inflammation; allergy;  
 KW autoimmune dysfunction.  
 OS Homo sapiens.  
 FH Key  
 FT peptide  
 FT 1. .22  
 FT /note= "Signal peptide"  
 FT protein  
 FT 23. .461  
 FT /note= "Mature hTNF-R"  
 FT peptide  
 FT 23. .185  
 FT /note= "Preferred soluble TNF-R"  
 FT peptide  
 FT 23. .207  
 FT /note= "Preferred soluble TNF-R"  
 FT peptide  
 FT 23. .257  
 FT /note= "Preferred soluble TNF-R"  
 FT peptide  
 FT 23. .206  
 FT /note= "Preferred soluble TNF-R"  
 FT peptide  
 FT 23. .204  
 FT /note= "Preferred soluble TNF-R"  
 FT peptide  
 FT 1. .206  
 FT /note= "Preferred soluble TNF-R"  
 FT peptide  
 FT 1. .204  
 FT /note= "Preferred soluble TNF-R"

WO9319777-A.  
 PD 14-OCT-1993.  
 PE 26-MAR-1993; U02938.  
 PR 30-MAR-1993; US-860710.  
 PA (IMV) IMMUNEX CORP.  
 PI Smith CA;  
 DR WPI; 93-336592/42.  
 DR N-PSDB; 049931.  
 PT New fusion protein tumour necrosis factor and human interleukin-1  
 PT receptor - useful in therapy, diagnosis and assays of e.g.  
 PT rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.  
 PS Claim 5; Fig 2; 85pp; English.  
 CC The sequences given in R42058-59 represent human tumour necrosis  
 CC factor receptor (TNF-R) and the sequences in R42060-61 represent  
 CC human interleukin-1 receptor (IL-1R). These sequences were used in



